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- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
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- <150> PCT/US00/04414  
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- <150> US 60/145,698  
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- <150> US 60/146,222  
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- <150> PCT/US99/20594  
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- <150> PCT/US99/20944  
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 Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
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090259-07001

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 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
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<212> PRT

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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| Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly | 100 | 105 | 110 |
| Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro | 115 | 120 | 125 |
| His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln | 130 | 135 | 140 |
| Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu | 145 | 150 | 155 |
| Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr | 165 | 170 | 175 |
| Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys | 180 | 185 | 190 |
| Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His | 195 | 200 | 205 |
| Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys | 210 | 215 | 220 |
| Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn | 225 | 230 | 235 |
| Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys | 245 | 250 | 255 |
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| Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys | 305 | 310 | 315 |
| His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His | 325 | 330 | 335 |
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FOOT 20 65220650

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 7

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<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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 oligonucleotide probe

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<212> PRT

<213> Homo sapiens

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
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Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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<223> Description of Artificial Sequence: Synthetic  
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<213> Homo sapiens

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

0902542050

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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

09902759-074001

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

FOOTNOTES 55220669

&lt;400&gt; 23

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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
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&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

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28

&lt;210&gt; 25

T00T20"65220660

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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<210> 27  
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 <212> DNA  
 <213> Homo sapiens

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 cttttttcct gaagtcttgg cttatcattt ccttggggct ctactcacag gtgtccaaac 360  
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09902759-071001

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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

09902759.071001



Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
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 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

09902759-071001

405 410 415  
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val  
 420 425 430  
 Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met  
 435 440 445  
 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly  
 450 455 460  
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
 465 470 475 480  
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu  
 485 490 495  
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala  
 500 505 510  
 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser  
 515 520 525  
 His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala  
 530 535 540  
 Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser  
 545 550 555 560  
 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys  
 565 570 575  
 Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly  
 580 585 590  
 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln  
 595 600 605  
 Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu  
 610 615 620  
 Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His  
 625 630 635 640  
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 His Cys His Thr  
 660

<210> 29  
 <211> 21  
 <212> DNA

090925-0700

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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0900259-01001

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| tgccccctctt | gctcgcccttg | aaaatggaaa  | agatgctcgc  | aggctgcttt  | ctgctgatcc  | 240  |
| tcggacagat  | cgtcctcctc  | cctgccgagg  | ccagggagcg  | gtcacgtggg  | aggtccatct  | 300  |
| ctagggggcag | acacgctcgg  | acccacccgc  | agacggccct  | tctggagagt  | tctgttgaga  | 360  |
| acaagcgggc  | agacctggtt  | ttcatcattg  | acagctctcg  | cagtgtcaac  | acccatgact  | 420  |
| atgcaaaggt  | caaggagttc  | atcgtggaca  | tcttgcaatt  | cttggacatt  | ggtcctgatg  | 480  |
| tcacccgagt  | gggcctgctc  | caatatggca  | gcactgtcaa  | gaatgagttc  | tccctcaaga  | 540  |
| ccttcaagag  | gaagtccgag  | gtggagcgtg  | ctgtcaagag  | gatgcggcat  | ctgtccacgg  | 600  |
| gcaccatgac  | tgggctggcc  | atccagtatg  | ccctgaacat  | cgcattctca  | gaagcagagg  | 660  |
| gggcccggcc  | cctgagggag  | aatgtgccac  | gggtcataat  | gatcgtgaca  | gatggggagac | 720  |
| ctcaggactc  | cgtggccgag  | gtggctgcta  | aggcacggga  | cacgggcatc  | ctaactcttg  | 780  |
| ccattggtgt  | gggccaggta  | gacttcaaca  | ccttgaagtc  | cattggggagt | gagccccatg  | 840  |
| aggaccatgt  | cttccttgtg  | gccaatttca  | gccagattga  | gacgctgacc  | tccgtgttcc  | 900  |
| agaagaagtt  | gtgcacggcc  | cacatgtgca  | gcaccctgga  | gcataactgt  | gcccacttct  | 960  |
| gcacaaacat  | ccctggctca  | tacgtctgca  | ggtgcaaaaca | aggctacatt  | ctcaactcgg  | 1020 |
| atcagacgac  | ttgcagaatc  | caggatctgt  | gtgccatgga  | ggaccacaac  | tgtgagcagc  | 1080 |
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| aggatgggaa  | gaggtgtgtg  | gctgtggact  | actgtgcctc  | agaaaaccac  | ggatgtgaac  | 1200 |
| atgagtgtgt  | aaatgctgat  | ggctcctacc  | tttgccagtg  | ccatgaagga  | tttgcctcta  | 1260 |
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| agggattccg  | gctcgctgag  | gatgggaaac  | gctgccgaag  | gaaggatgtc  | tgcaaatcaa  | 1920 |
| cccaccatgg  | ctgcgaacac  | atttgtgtta  | ataatgggaa  | ttcctacatc  | tgcaaatgct  | 1980 |
| cagagggatt  | tgttctagct  | gaggacggaa  | gacgggtgcaa | gaaatgcact  | gaaggcccaa  | 2040 |
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| gaacgcagtg  | cagagcccca  | aagctcaggc  | tattgttaaa  | tcaataatgt  | tgtgaagtaa  | 3060 |
| aacaatcagt  | actgagaaac  | ctggtttgcc  | acagaacaaa  | gacaagaagt  | atacactaac  | 3120 |
| ttgtataaat  | ttatctagga  | aaaaaatcct  | tcagaattct  | aagatgaatt  | taccaggtga  | 3180 |
| gaatgaataa  | gctatgcaag  | gtattttgtg  | atatactgtg  | gacacaactt  | gcttctgcct  | 3240 |
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<210> 34
<211> 915
<212> PRT
<213> Homo sapiens
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| <400> 34 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met      | Glu | Lys | Met | Leu | Ala | Gly | Cys | Phe | Leu | Leu | Ile | Leu | Gly | Gln | Ile |
| 1        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val      | Leu | Leu | Pro | Ala | Glu | Ala | Arg | Glu | Arg | Ser | Arg | Gly | Arg | Ser | Ile |
|          |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser      | Arg | Gly | Arg | His | Ala | Arg | Thr | His | Pro | Gln | Thr | Ala | Leu | Leu | Glu |
|          |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser      | Ser | Cys | Glu | Asn | Lys | Arg | Ala | Asp | Leu | Val | Phe | Ile | Ile | Asp | Ser |
|          | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser      | Arg | Ser | Val | Asn | Thr | His | Asp | Tyr | Ala | Lys | Val | Lys | Glu | Phe | Ile |
| 65       |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val      | Asp | Ile | Leu | Gln | Phe | Leu | Asp | Ile | Gly | Pro | Asp | Val | Thr | Arg | Val |
|          |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly      | Leu | Leu | Gln | Tyr | Gly | Ser | Thr | Val | Lys | Asn | Glu | Phe | Ser | Leu | Lys |
|          |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr      | Phe | Lys | Arg | Lys | Ser | Glu | Val | Glu | Arg | Ala | Val | Lys | Arg | Met | Arg |
|          |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His      | Leu | Ser | Thr | Gly | Thr | Met | Thr | Gly | Leu | Ala | Ile | Gln | Tyr | Ala | Leu |
|          | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn      | Ile | Ala | Phe | Ser | Glu | Ala | Glu | Gly | Ala | Arg | Pro | Leu | Arg | Glu | Asn |
| 145      |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val      | Pro | Arg | Val | Ile | Met | Ile | Val | Thr | Asp | Gly | Arg | Pro | Gln | Asp | Ser |
|          |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val      | Ala | Glu | Val | Ala | Ala | Lys | Ala | Arg | Asp | Thr | Gly | Ile | Leu | Ile | Phe |
|          |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala      | Ile | Gly | Val | Gly | Gln | Val | Asp | Phe | Asn | Thr | Leu | Lys | Ser | Ile | Gly |
|          |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser      | Glu | Pro | His | Glu | Asp | His | Val | Phe | Leu | Val | Ala | Asn | Phe | Ser | Gln |
|          | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile      | Glu | Thr | Leu | Thr | Ser | Val | Phe | Gln | Lys | Lys | Leu | Cys | Thr | Ala | His |

|                 |                     |                 |                 |     |  |     |
|-----------------|---------------------|-----------------|-----------------|-----|--|-----|
| 225             |                     | 230             |                 | 235 |  | 240 |
| Met Cys Ser Thr | Leu Glu His Asn Cys | Ala His Phe Cys | Ile Asn Ile     |     |  |     |
|                 | 245                 | 250             | 255             |     |  |     |
| Pro Gly Ser Tyr | Val Cys Arg Cys     | Lys Gln Gly Tyr | Ile Leu Asn Ser |     |  |     |
|                 | 260                 | 265             | 270             |     |  |     |
| Asp Gln Thr Thr | Cys Arg Ile Gln Asp | Leu Cys Ala Met | Glu Asp His     |     |  |     |
|                 | 275                 | 280             | 285             |     |  |     |
| Asn Cys Glu Gln | Leu Cys Val Asn Val | Pro Gly Ser Phe | Val Cys Gln     |     |  |     |
|                 | 290                 | 295             | 300             |     |  |     |
| Cys Tyr Ser Gly | Tyr Ala Leu Ala     | Glu Asp Gly Lys | Arg Cys Val Ala |     |  |     |
| 305             | 310                 | 315             | 320             |     |  |     |
| Val Asp Tyr Cys | Ala Ser Glu Asn His | Gly Cys Glu His | Glu Cys Val     |     |  |     |
|                 | 325                 | 330             | 335             |     |  |     |
| Asn Ala Asp Gly | Ser Tyr Leu Cys     | Gln Cys His Glu | Gly Phe Ala Leu |     |  |     |
|                 | 340                 | 345             | 350             |     |  |     |
| Asn Pro Asp Glu | Lys Thr Cys Thr     | Arg Ile Asn Tyr | Cys Ala Leu Asn |     |  |     |
|                 | 355                 | 360             | 365             |     |  |     |
| Lys Pro Gly Cys | Glu His Glu Cys     | Val Asn Met Glu | Glu Ser Tyr Tyr |     |  |     |
|                 | 370                 | 375             | 380             |     |  |     |
| Cys Arg Cys His | Arg Gly Tyr Thr     | Leu Asp Pro Asn | Gly Lys Thr Cys |     |  |     |
| 385             | 390                 | 395             | 400             |     |  |     |
| Ser Arg Val Asp | His Cys Ala Gln     | Gln Asp His Gly | Cys Glu Gln Leu |     |  |     |
|                 | 405                 | 410             | 415             |     |  |     |
| Cys Leu Asn Thr | Glu Asp Ser Phe     | Val Cys Gln Cys | Ser Glu Gly Phe |     |  |     |
|                 | 420                 | 425             | 430             |     |  |     |
| Leu Ile Asn Glu | Asp Leu Lys Thr     | Cys Ser Arg Val | Asp Tyr Cys Leu |     |  |     |
|                 | 435                 | 440             | 445             |     |  |     |
| Leu Ser Asp His | Gly Cys Glu Tyr     | Ser Cys Val Asn | Met Asp Arg Ser |     |  |     |
|                 | 450                 | 455             | 460             |     |  |     |
| Phe Ala Cys Gln | Cys Pro Glu Gly     | His Val Leu Arg | Ser Asp Gly Lys |     |  |     |
| 465             | 470                 | 475             | 480             |     |  |     |
| Thr Cys Ala Lys | Leu Asp Ser Cys     | Ala Leu Gly Asp | His Gly Cys Glu |     |  |     |
|                 | 485                 | 490             | 495             |     |  |     |
| His Ser Cys Val | Ser Ser Glu Asp     | Ser Phe Val Cys | Gln Cys Phe Glu |     |  |     |
|                 | 500                 | 505             | 510             |     |  |     |

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 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
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 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
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 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
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 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
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 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
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 770 775 780  
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 785 790 795 800

09902759-071001

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
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Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
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Arg Tyr Arg  
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<211> 23

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

09902759-071001



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

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45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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tttgatatgaa aaa 1813

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&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln | 20  | 25  | 30  |
| Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val | 35  | 40  | 45  |
| Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln | 50  | 55  | 60  |
| Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys | 65  | 70  | 75  |
| Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro | 85  | 90  | 95  |
| Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg | 100 | 105 | 110 |
| Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val | 115 | 120 | 125 |
| Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr | 130 | 135 | 140 |
| Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu | 145 | 150 | 155 |
| Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser | 165 | 170 | 175 |
| Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro | 180 | 185 | 190 |
| Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser | 195 | 200 | 205 |
| Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys | 210 | 215 | 220 |
| Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu | 225 | 230 | 235 |
| Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly | 245 | 250 | 255 |
| Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His | 260 | 265 | 270 |
| Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp | 275 | 280 | 285 |

09902759.074001

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
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<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

0590259.07104

<400> 42  
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 <210> 43  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
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 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
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 <210> 46  
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090259-0101  
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<211> 45  
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<220>  
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 oligonucleotide probe

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<210> 48  
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 <213> Homo sapiens

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<210> 49
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<212> PRT
<213> Homo sapiens

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      20             25            30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35             40            45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50             55            60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65             70            75            80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85             90            95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100            105            110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115            120            125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130            135            140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145            150            155            160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165            170            175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
|   | 180 |     | 185 |     | 190 |
| Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val | 195 | 200 | 205 |     |     |
| Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys | 210 | 215 | 220 |     |     |
| Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe | 225 | 230 | 235 | 240 |     |
| Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys | 245 | 250 | 255 |     |     |
| Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met | 260 | 265 | 270 |     |     |
| Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala | 275 | 280 | 285 |     |     |
| Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser | 290 | 295 | 300 |     |     |
| Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln | 305 | 310 | 315 | 320 |     |
| Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile | 325 | 330 | 335 |     |     |
| Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys | 340 | 345 | 350 |     |     |
| Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser | 355 | 360 | 365 |     |     |
| Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp | 370 | 375 | 380 |     |     |
| Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser | 385 | 390 | 395 | 400 |     |
| Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly | 405 | 410 | 415 |     |     |
| Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln | 420 | 425 | 430 |     |     |
| Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr | 435 | 440 | 445 |     |     |
| Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys | 450 | 455 | 460 |     |     |

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Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525  
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540  
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575  
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605  
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620  
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655  
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670  
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685

Leu Arg  
 690

<210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (61)

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<223> a, t, c or g

<400> 50

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gtattgggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
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gatagggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
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tataatatcc ttacaaggat cactcaacta ggaataatta ttccactgat ttgtcttgcc 540
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

095025-01001  
T00T00-052050

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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cgctaagcga ggctcctcc tcccgcagat ccgaacggcc tgggcgggggt caccgccgct 120

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gggacaagaa gccgcccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcccggg gcggaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctaccctgtg ggcccgttaag gcgctactat ataaggctgc 300  
 cggcccggag ccgcgcgcgc gtcagagcag gagcgtgctg tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca gcgcatcccg gtcgcccggc agcctcccgc 420  
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 gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040  
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

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Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgcccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctccccgt ctccctgagc agtgccaaac agcggcagtg ta

42

 090259-071001  
 TOT 2.0" 65420650

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

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 gctgctgctg cgctacctgg tggcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240  
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 tttcaatata cggatcaaaa atgtgacaag aagtgtgctg gggaaatata gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
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 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

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Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                   35                                  40                                  45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
                   50                                  55                                  60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
                   65                                  70                                  75                                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                                   85                                  90                                  95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                                   100                                  105                                  110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                                   115                                  120                                  125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
                   130                                  135                                  140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
                   145                                  150                                  155                                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                                   165                                  170                                  175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                                   180                                  185                                  190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                                   195                                  200                                  205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
                   210                                  215                                  220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
                   225                                  230                                  235                                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                                   245                                  250                                  255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                                   260                                  265                                  270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                                   275                                  280                                  285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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 Gly Gly Ser Arg Gly Gln Glu Phe

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305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgatga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
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FOOTNOTES 5220660

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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 340 |     |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |  |
| Thr | Ile | Glu | Ser | Leu | Pro | Asn | Leu | Lys | Glu | Ile | Ser | Ile | His | Ser | Asn |     |  |
| 355 |     |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |  |
| Pro | Ile | Arg | Cys | Asp | Cys | Val | Ile | Arg | Trp | Met | Asn | Met | Asn | Lys | Thr |     |  |
| 370 |     |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Asn | Ile | Arg | Phe | Met | Glu | Pro | Asp | Ser | Leu | Phe | Cys | Val | Asp | Pro | Pro |     |  |
| 385 |     |     |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |  |
| Glu | Phe | Gln | Gly | Gln | Asn | Val | Arg | Gln | Val | His | Phe | Arg | Asp | Met | Met |     |  |
| 405 |     |     |     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     |  |
| Glu | Ile | Cys | Leu | Pro | Leu | Ile | Ala | Pro | Glu | Ser | Phe | Pro | Ser | Asn | Leu |     |  |
| 420 |     |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     |  |
| Asn | Val | Glu | Ala | Gly | Ser | Tyr | Val | Ser | Phe | His | Cys | Arg | Ala | Thr | Ala |     |  |
| 435 |     |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |  |
| Glu | Pro | Gln | Pro | Glu | Ile | Tyr | Trp | Ile | Thr | Pro | Ser | Gly | Gln | Lys | Leu |     |  |
| 450 |     |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Leu | Pro | Asn | Thr | Leu | Thr | Asp | Lys | Phe | Tyr | Val | His | Ser | Glu | Gly | Thr |     |  |
| 465 |     |     |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |  |
| Leu | Asp | Ile | Asn | Gly | Val | Thr | Pro | Lys | Glu | Gly | Gly | Leu | Tyr | Thr | Cys |     |  |
| 485 |     |     |     |     |     |     | 490 |     |     |     |     | 495 |     |     |     |     |  |
| Ile | Ala | Thr | Asn | Leu | Val | Gly | Ala | Asp | Leu | Lys | Ser | Val | Met | Ile | Lys |     |  |
| 500 |     |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |     |  |
| Val | Asp | Gly | Ser | Phe | Pro | Gln | Asp | Asn | Asn | Gly | Ser | Leu | Asn | Ile | Lys |     |  |
| 515 |     |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |     |  |
| Ile | Arg | Asp | Ile | Gln | Ala | Asn | Ser | Val | Leu | Val | Ser | Trp | Lys | Ala | Ser |     |  |
| 530 |     |     |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |
| Ser | Lys | Ile | Leu | Lys | Ser | Ser | Val | Lys | Trp | Thr | Ala | Phe | Val | Lys | Thr |     |  |
| 545 |     |     |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |  |
| Glu | Asn | Ser | His | Ala | Ala | Gln | Ser | Ala | Arg | Ile | Pro | Ser | Asp | Val | Lys |     |  |
| 565 |     |     |     |     |     |     | 570 |     |     |     |     | 575 |     |     |     |     |  |
| Val | Tyr | Asn | Leu | Thr | His | Leu | Asn | Pro | Ser | Thr | Glu | Tyr | Lys | Ile | Cys |     |  |
| 580 |     |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |     |     |  |
| Ile | Asp | Ile | Pro | Thr | Ile | Tyr | Gln | Lys | Asn | Arg | Lys | Lys | Cys | Val | Asn |     |  |
| 595 |     |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |     |  |
| Val | Thr | Thr | Lys | Gly | Leu | His | Pro | Asp | Gln | Lys | Glu | Tyr | Glu | Lys | Asn |     |  |
| 610 |     |     |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taacccgttc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctctct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgct 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttcctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780
taccgattat gccatgctgg tcacctgtt tggctggttc actatggtga tctcatatgt 840
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cacccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

T00T20"55220660

15



Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

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0502001



<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

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 100140-6520660

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccagggag cgggcccggga agcgcgatgg gggccccagc cgctcgcctc ctgctcctgc 180  
 tctgtctgtt cgcttgcctg tgggcgccc gcggggcca cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
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 tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcgggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttatata 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgaggggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctccctttc ctcaacaaga 1020  
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 acacctcaa tgtaaatgac cccagtcggg tgcctcctc ctccagcacc taccacgcca 1140  
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 gccactactt gatccggcac aaaggaaact acctgacaca tgaggcaaaa ggctccgacg 1260  
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 cctttccgt ggcttctctg catttggtt attattatt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

0902259.01001

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
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 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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## oligonucleotide probe

<400> 87  
 cctagcacag tgacgagggga cttggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 88  
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 89  
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
 <211> 2755  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
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 gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180  
 tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240  
 agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaaa 300  
 gggcttcaca agtctgcagc gtttcaactgc cccgacttcc cagttttacc atttatttct 360  
 gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggg 420  
 tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccggggggctt ttctggggct 480  
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 agaccggggg gccttcagg acttgaacaa gctggagggtg ctcatthtaa atgacaatct 660  
 catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tgcacctccg 720  
 gggtaacagg ctgaaaacgc tgccctatga ggaggtcttg gagcaaatac ctggtattgc 780  
 ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840  
 atggctggaa aacattccca agaatgccct gatcggccga gtggtctgcg aagccccac 900  
 cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960  
 ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagacctttg ctctgggacc 1020  
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 T00T20-5520660

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<210> 91
<211> 696
<212> PRT
<213> Homo sapiens
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<400> 91
Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1             5             10             15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20             25             30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35             40             45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50             55             60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65             70             75             80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85             90             95

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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
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 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

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Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

FOOTNOTES 220560



660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttggatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgatgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95  
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gctgcaccgg gcttggcagc gctccgcaca catttctgt cgcggcctaa gggaaactgt 120  
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180

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gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
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 aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160  
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 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

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Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
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 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

09902759.071004

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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 97  
tggaaggaga tgcgatgccca cctg

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<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence
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<400> 98  
tgaccagtgg ggaaggacag

20

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga gggcgccttg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 101  
 tcaggaagg agtgtgcagt tctg 24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

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&lt;400&gt; 103

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aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

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&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

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Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Asn | Met | Ser | Ala | Arg | Leu | Thr | Val | Val | Cys | Lys | Gln | Cys | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Leu | Arg | Arg | Gly | Leu | Asn | Tyr | Ile | Ile | Met | Gly | Gln | Val | Gly | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Gly | Arg | Gly | Lys | Ile | Met | Pro | Asn | Ser | Phe | Ile | Met | Met | Phe | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Lys | Asn | Gln | Lys | Leu | Leu | Asp | Ala | Leu | Lys | Asn | Lys | Gln | Cys |     |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

0990259.071001



<213> Homo sapiens

<400> 108

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cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
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aagggcctag tcccagctgt gctctggggc ctacgctct tctcaacct cccaggacct 180
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ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
    20           25           30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
    35           40           45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
    50           55           60

```

F00F20"6520660

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

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Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365  
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
       370                                  375                                  380  
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400  
 Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415  
 Ile Lys Gly Arg  
                                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

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<220>  
<221> modified_base  
<222> (1461)  
<223> a, t, c or g
```

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<210> 114
<211> 366
<212> PRT
<213> Homo sapiens
```

<400> 114  
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
1 5 10 15  
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
20 25 30  
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

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Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgccca taacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttag aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccage accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

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```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggg tcaaagatgg gatagtgat cctacgaatc caaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tggctcttga tcccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggcatcgtt ggcagccgtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtccccgaa gtgaaggaga attcaaacag acctcgtcat tcctgggtgt agcctgggtc 960
gctcaccgcc tatcatctgc atttgcttca ctcagggtgt accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
tttccctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
ctctgcccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt gtggagagca tagtaaat ttagagaact tgaagccaaa aggattttaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10             15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85              90              95

```

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Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctggt tccc

24

<210> 121

<211> 50

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**000000000000**

## oligonucleotide probe

<400> 125  
 actcagcagt ggtaggaaag 20

<210> 126  
 <211> 1210  
 <212> DNA  
 <213> Homo sapiens

<400> 126  
 cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60  
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120  
 gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
 gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
 ggattgagcc atgtaccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccc 360  
 gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
 tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
 ggcgtgcgga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
 atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
 tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgccccct 660  
 ctgtcgggaa tgccacatcc tccctgcgcg gagaccagtc tgggaagcca actgcctatg 720  
 gggttattgc agctgctgcg gtgctcagtg caagcctggg caccgccacc ctccctcttt 780  
 tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggg gccatgaagg 840  
 agtcctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
 ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtacct 960  
 gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccgcagc 1020  
 tccctcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
 agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
 ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
 aagttgcttc 1210

<210> 127  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 127  
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
 1 5 10 15  
 Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
 20 25 30  
 Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
 35 40 45  
 Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
 50 55 60  
 Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
 65 70 75 80

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 10012015220660

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cgggtctcgtc cgctcgcgca gcggcggcag cagagggtcgc gcacagatgc 60  
 gggtttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccggt cattcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccocgacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgtgtgtt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctgggt gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttggtgag cgctacaacc 960  
 acggaactgt ggtggagttt tactgcgata ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatac 1080  
 agcaaacgtg gccacgaccc catgagaccc tcttgaccac gtggaagatt gtggcggttca 1140

cggcaaccag tgtgctgctg gtgctgctgc tegtcatcct ggccaggatg ttccagacca 1200  
 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gacctgact 1260  
 ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320  
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 tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gtcctaaagt ctgtattcac 1500  
 ctcccagggtg ccaagagagc acccacctg cttcggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620  
 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgataccta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtctt 1800  
 gttttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

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| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ile | Ser | Glu | Leu | Gln | Thr | Ser | Phe | Pro | Val | Gly | Thr | Val | Ile | Ser | Tyr |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Arg | Cys | Phe | Pro | Gly | Phe | Lys | Leu | Asp | Gly | Ser | Ala | Tyr | Leu | Glu | Cys |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Leu | Gln | Asn | Leu | Ile | Trp | Ser | Ser | Ser | Pro | Pro | Arg | Cys | Leu | Ala | Leu |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Glu | Ala | Gln | Val | Cys | Pro | Leu | Pro | Pro | Met | Val | Ser | His | Gly | Asp | Phe |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |
| Val | Cys | His | Pro | Arg | Pro | Cys | Glu | Arg | Tyr | Asn | His | Gly | Thr | Val | Val |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Glu | Phe | Tyr | Cys | Asp | Pro | Gly | Tyr | Ser | Leu | Thr | Ser | Asp | Tyr | Lys | Tyr |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Ile | Thr | Cys | Gln | Tyr | Gly | Glu | Trp | Phe | Pro | Ser | Tyr | Gln | Val | Tyr | Cys |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Ile | Lys | Ser | Glu | Gln | Thr | Trp | Pro | Ser | Thr | His | Glu | Thr | Leu | Leu | Thr |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |
| Thr | Trp | Lys | Ile | Val | Ala | Phe | Thr | Ala | Thr | Ser | Val | Leu | Leu | Val | Leu |  |  |  |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |  |  |
| Leu | Leu | Val | Ile | Leu | Ala | Arg | Met | Phe | Gln | Thr | Lys | Phe | Lys | Ala | His |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |
| Phe | Pro | Pro | Arg | Gly | Pro | Pro | Arg | Ser | Ser | Ser | Ser | Asp | Pro | Asp | Phe |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |
| Val | Val | Val | Asp | Gly | Val | Pro | Val | Met | Leu | Pro | Ser | Tyr | Asp | Glu | Ala |  |  |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Val | Ser | Gly | Gly | Leu | Ser | Ala | Leu | Gly | Pro | Gly | Tyr | Met | Ala | Ser | Val |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |
| Gly | Gln | Gly | Cys | Pro | Leu | Pro | Val | Asp | Asp | Gln | Ser | Pro | Pro | Ala | Tyr |  |  |  |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |
| Pro | Gly | Ser | Gly | Asp | Thr | Asp | Thr | Gly | Pro | Gly | Glu | Ser | Glu | Thr | Cys |  |  |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |  |
| Asp | Ser | Val | Ser | Gly | Ser | Ser | Glu | Leu | Leu | Gln | Ser | Leu | Tyr | Ser | Pro |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |
| Pro | Arg | Cys | Gln | Glu | Ser | Thr | His | Pro | Ala | Ser | Asp | Asn | Pro | Asp | Ile |  |  |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |

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Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtcgcgtc gtggcctaga 60  
gatgctgctg ccgcgggttg agttgtcgcg cagcctctg ccgcagcc cgctccaccg 120  
ccgtagcgcg cgagtgtcgg ggggcgcacc cgagtgcggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
tgagtgcctc ggatttgac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

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ggcccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360  
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 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tccctgcccga 600  
 gcgaggctcg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggccccct 660  
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 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctcctcctcc 900  
 ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
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 aaatgtcact tgggtgggtt tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtacacagc 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110

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Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

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<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccgcg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactctg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcggaatc tggagtcac cggttgtttg ctggctgggc ttttccagtg 720

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tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780  
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 ttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaaacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtagggcc 1080  
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260  
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 ggtgccgaga gggtgcctg atgggctctg cccgctggac atgttcttga atgcatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttggaat gaagagtaac tgatttataa aagcaggatg tggtgatttt aaaataaagt 1500  
 gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
 1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
 165 170 175

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Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
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 agctgccagc ggaacccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360  
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 agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480  
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 gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
 cctccgggccc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660  
 aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720  
 ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780  
 caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840  
 aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900  
 ctgtgatgac aactggggag aaaaggagga ccagggtgga tgcaagcaac tgggctgtgg 960  
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 attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgt 1140  
 ggtgggcatc atctaactct ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200  
 atttactgtc tacatgactg catgggatga aactgatct tcttctgccc ttggactggg 1260  
 acttataact ggtgcccctg attctcagge cttcagagtt ggatcagaac ttacaacatc 1320  
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 acggaatttt aaggataaat tttctgaatt gggttatggg tttctgaaat tggtctata 1620  
 atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680  
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
 100 105 110

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Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
           115                          120                          125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
       130                          135                          140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
   145                          150                          155                          160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
                           165                          170                          175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
                           180                          185                          190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
           195                          200                          205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
       210                          215                          220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
   225                          230                          235                          240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
                           245                          250                          255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
                           260                          265                          270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
       275                          280                          285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
       290                          295                          300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
   305                          310                          315                          320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
                           325                          330                          335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
           340                          345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
 acccacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120  
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggtcggctg 180  
 cctgggcgct ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctcagggtcg ggcaaagaat gtgcaaaagt 300  
 cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480  
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggccaggt 600  
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 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720  
 gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780  
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 ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900  
 ggtggccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
 cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

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agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140  
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 gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260  
 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380  
 cttggccgcc atggcccaac ttgtttattg cagcttataa tgggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala  
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

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|   |     |         |
|---|-----|---------|
| 210   | 215 | 220     |
| Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg |     |         |
| 225   | 230 | 235 240 |
| Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu |     |         |
|   | 245 | 250 255 |
| Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val |     |         |
|   | 260 | 265 270 |
| Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu |     |         |
|   | 275 | 280 285 |
| Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu |     |         |
|   | 290 | 295 300 |

Arg Lys Ser Lys Asn Ser  
305 310

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154  
ggtgctaaac tgggtgctctg tggc

24

<210> 155  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155  
cagggcaaga tgagcattcc

20

<210> 156  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

09902759.071001

<400> 156  
tcatactgtt ccatactcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtgggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcattg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaacacgc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataccttt gtggttagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaataaat gctgggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat tttattcca tcttctatag cttttttaac 900  
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1771

<210> 159

0990259.0101  
100720-55220660

<211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 159

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Leu | Leu | Asp | Ile | Leu | Leu | Leu | Leu | Pro | Leu | Leu | Ile | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Leu | Glu | Ser | Phe | Val | Lys | Leu | Phe | Ile | Pro | Lys | Arg | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Thr | Gly | Glu | Ile | Val | Leu | Ile | Thr | Gly | Ala | Gly | His | Gly | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Arg | Leu | Thr | Ala | Tyr | Glu | Phe | Ala | Lys | Leu | Lys | Ser | Lys | Leu | Val |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Trp | Asp | Ile | Asn | Lys | His | Gly | Leu | Glu | Glu | Thr | Ala | Ala | Lys | Cys |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Gly | Leu | Gly | Ala | Lys | Val | His | Thr | Phe | Val | Val | Asp | Cys | Ser | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Glu | Asp | Ile | Tyr | Ser | Ser | Ala | Lys | Lys | Val | Lys | Ala | Glu | Ile | Gly |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Ser | Ile | Leu | Val | Asn | Asn | Ala | Gly | Val | Val | Tyr | Thr | Ser | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Phe | Ala | Thr | Gln | Asp | Pro | Gln | Ile | Glu | Lys | Thr | Phe | Glu | Val | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Ala | His | Phe | Trp | Thr | Thr | Lys | Ala | Phe | Leu | Pro | Ala | Met | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asn | Asn | His | Gly | His | Ile | Val | Thr | Val | Ala | Ser | Ala | Ala | Gly | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ser | Val | Pro | Phe | Leu | Leu | Ala | Tyr | Cys | Ser | Ser | Lys | Phe | Ala | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gly | Phe | His | Lys | Thr | Leu | Thr | Asp | Glu | Leu | Ala | Ala | Leu | Gln | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Gly | Val | Lys | Thr | Thr | Cys | Leu | Cys | Pro | Asn | Phe | Val | Asn | Thr | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Lys | Asn | Pro | Ser | Thr | Ser | Leu | Gly | Pro | Thr | Leu | Glu | Pro | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Val | Val | Asn | Arg | Leu | Met | His | Gly | Ile | Leu | Thr | Glu | Gln | Lys | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

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Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
                   260                  265                  270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
           275                  280                  285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
       290                  295                  300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggaacgc tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

090275.071001

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
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 caggggtggc cgggaggttc atccatgttt ggactccttg tggaacatgg gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
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 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcctttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
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 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560  
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 ttttaggggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980  
 ataatagttt tggggaaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Lys | Thr | Tyr | Asn | Ser | Asn | Leu | Phe | Phe | Trp | Phe | Phe | Pro | Ala | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Gln | Pro | Glu | Asp | Ala | Pro | Val | Val | Leu | Trp | Leu | Gln | Gly | Gly | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Ser | Ser | Met | Phe | Gly | Leu | Phe | Val | Glu | His | Gly | Pro | Tyr | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Thr | Ser | Asn | Met | Thr | Leu | Arg | Asp | Arg | Asp | Phe | Pro | Trp | Thr | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Ser | Met | Leu | Tyr | Ile | Asp | Asn | Pro | Val | Gly | Thr | Gly | Phe | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Thr | Asp | Asp | Thr | His | Gly | Tyr | Ala | Val | Asn | Glu | Asp | Asp | Val | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Asp | Leu | Tyr | Ser | Ala | Leu | Ile | Gln | Phe | Phe | Gln | Ile | Phe | Pro | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Lys | Asn | Asn | Asp | Phe | Tyr | Val | Thr | Gly | Glu | Ser | Tyr | Ala | Gly | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Val | Pro | Ala | Ile | Ala | His | Leu | Ile | His | Ser | Leu | Asn | Pro | Val | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Val | Lys | Ile | Asn | Leu | Asn | Gly | Ile | Ala | Ile | Gly | Asp | Gly | Tyr | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Pro | Glu | Ser | Ile | Ile | Gly | Gly | Tyr | Ala | Glu | Phe | Leu | Tyr | Gln | Ile |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gly | Leu | Leu | Asp | Glu | Lys | Gln | Lys | Lys | Tyr | Phe | Gln | Lys | Gln | Cys | His |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Cys | Ile | Glu | His | Ile | Arg | Lys | Gln | Asn | Trp | Phe | Glu | Ala | Phe | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Leu | Asp | Lys | Leu | Leu | Asp | Gly | Asp | Leu | Thr | Ser | Asp | Pro | Ser | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Gln | Asn | Val | Thr | Gly | Cys | Ser | Asn | Tyr | Tyr | Asn | Phe | Leu | Arg | Cys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Glu | Pro | Glu | Asp | Gln | Leu | Tyr | Tyr | Val | Lys | Phe | Leu | Ser | Leu | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Val | Arg | Gln | Ala | Ile | His | Val | Gly | Asn | Gln | Thr | Phe | Asn | Asp | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

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Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tg gatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

FOOT-0-65220550



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 167

agctctcaga ggctgggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 168

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50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

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agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaga 2340  
aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400  
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

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Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

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Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
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 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
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 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

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450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

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20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

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24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
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<223> a, t, c or g

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tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctgggtccctc 180  
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ggaggggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccccct 480  
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tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgcca ccatcaactt gcagtcaaca cagagctgc 840  
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20                      25                      30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
          35                      40                      45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
          50                      55                      60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
          65                      70                      75                      80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85                      90                      95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
          100                      105                      110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
          115                      120                      125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
          130                      135                      140

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Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
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 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

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Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
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Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
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<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu

1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val

20 25 30

Asp Arg Gly His Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Leu | Leu | Lys | Met | Arg | Trp | Ser | Gly | Leu | Asn | Ala | Ile | Gln | Phe | 65  | 70  | 75  | 80  |
| Tyr | Val | Pro | Trp | Asn | Tyr | His | Glu | Pro | Gln | Pro | Gly | Val | Tyr | Asn | Phe | 85  | 90  | 95  |     |
| Asn | Gly | Ser | Arg | Asp | Leu | Ile | Ala | Phe | Leu | Asn | Glu | Ala | Ala | Leu | Ala | 100 | 105 | 110 |     |
| Asn | Leu | Leu | Val | Ile | Leu | Arg | Pro | Gly | Pro | Tyr | Ile | Cys | Ala | Glu | Trp | 115 | 120 | 125 |     |
| Glu | Met | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Arg | Lys | Pro | Glu | Ile | His | 130 | 135 | 140 |     |
| Leu | Arg | Thr | Ser | Asp | Pro | Asp | Phe | Leu | Ala | Ala | Val | Asp | Ser | Trp | Phe | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Leu | Pro | Lys | Ile | Tyr | Pro | Trp | Leu | Tyr | His | Asn | Gly | Gly | 165 | 170 | 175 |     |
| Asn | Ile | Ile | Ser | Ile | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Arg | Ala | 180 | 185 | 190 |     |
| Cys | Asp | Phe | Ser | Tyr | Met | Arg | His | Leu | Ala | Gly | Leu | Phe | Arg | Ala | Leu | 195 | 200 | 205 |     |
| Leu | Gly | Glu | Lys | Ile | Leu | Leu | Phe | Thr | Thr | Asp | Gly | Pro | Glu | Gly | Leu | 210 | 215 | 220 |     |
| Lys | Cys | Gly | Ser | Leu | Arg | Gly | Leu | Tyr | Thr | Thr | Val | Asp | Phe | Gly | Pro | 225 | 230 | 235 | 240 |
| Ala | Asp | Asn | Met | Thr | Lys | Ile | Phe | Thr | Leu | Leu | Arg | Lys | Tyr | Glu | Pro | 245 | 250 | 255 |     |
| His | Gly | Pro | Leu | Val | Asn | Ser | Glu | Tyr | Tyr | Thr | Gly | Trp | Leu | Asp | Tyr | 260 | 265 | 270 |     |
| Trp | Gly | Gln | Asn | His | Ser | Thr | Arg | Ser | Val | Ser | Ala | Val | Thr | Lys | Gly | 275 | 280 | 285 |     |
| Leu | Glu | Asn | Met | Leu | Lys | Leu | Gly | Ala | Ser | Val | Asn | Met | Tyr | Met | Phe | 290 | 295 | 300 |     |
| His | Gly | Gly | Thr | Asn | Phe | Gly | Tyr | Trp | Asn | Gly | Ala | Asp | Lys | Lys | Gly | 305 | 310 | 315 | 320 |
| Arg | Phe | Leu | Pro | Ile | Thr | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Pro | Ile | Ser | 325 | 330 | 335 |     |
| Glu | Ala | Gly | Asp | Pro | Thr | Pro | Lys | Leu | Phe | Ala | Leu | Arg | Asp | Val | Ile |     |     |     |     |

FOOT 20" 65220660

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 340 |     |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ser | Lys | Phe | Gln | Glu | Val | Pro | Leu | Gly | Pro | Leu | Pro | Pro | Pro | Ser | Pro |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Met | Met | Leu | Gly | Pro | Val | Thr | Leu | His | Leu | Val | Gly | His | Leu | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Phe | Leu | Asp | Leu | Leu | Cys | Pro | Arg | Gly | Pro | Ile | His | Ser | Ile | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Met | Thr | Phe | Glu | Ala | Val | Lys | Gln | Asp | His | Gly | Phe | Met | Leu | Tyr |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Arg | Thr | Tyr | Met | Thr | His | Thr | Ile | Phe | Glu | Pro | Thr | Pro | Phe | Trp | Val |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Pro | Asn | Asn | Gly | Val | His | Asp | Arg | Ala | Tyr | Val | Met | Val | Asp | Gly | Val |
|     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |
| Phe | Gln | Gly | Val | Val | Glu | Arg | Asn | Met | Arg | Asp | Lys | Leu | Phe | Leu | Thr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Lys | Leu | Gly | Ser | Lys | Leu | Asp | Ile | Leu | Val | Glu | Asn | Met | Gly | Arg |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Ser | Phe | Gly | Ser | Asn | Ser | Ser | Asp | Phe | Lys | Gly | Leu | Leu | Lys | Pro |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Pro | Ile | Leu | Gly | Gln | Thr | Ile | Leu | Thr | Gln | Trp | Met | Met | Phe | Pro | Leu |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Lys | Ile | Asp | Asn | Leu | Val | Lys | Trp | Trp | Phe | Pro | Leu | Gln | Leu | Pro | Lys |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Trp | Pro | Tyr | Pro | Gln | Ala | Pro | Ser | Gly | Pro | Thr | Phe | Tyr | Ser | Lys | Thr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Phe | Pro | Ile | Leu | Gly | Ser | Val | Gly | Asp | Thr | Phe | Leu | Tyr | Leu | Pro | Gly |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Trp | Thr | Lys | Gly | Gln | Val | Trp | Ile | Asn | Gly | Phe | Asn | Leu | Gly | Arg | Tyr |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Trp | Thr | Lys | Gln | Gly | Pro | Gln | Gln | Thr | Leu | Tyr | Val | Pro | Arg | Phe | Leu |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Leu | Phe | Pro | Arg | Gly | Ala | Leu | Asn | Lys | Ile | Thr | Leu | Leu | Glu | Leu | Glu |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Asp | Val | Pro | Leu | Gln | Pro | Gln | Val | Gln | Phe | Leu | Asp | Lys | Pro | Ile | Leu |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattat 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcaattgaga tgccctcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg attttaaagt caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag cttttaaacc gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattacc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatagct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatactact gggaacaaag tggacattct gccaaaacaa ttgttttaaa 1320

090254.001  
 15.220660



Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

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465                                      470                                      475                                      480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

   485                                      490                                      495

Phe Ala Asn Gly Ile

   500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c 21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg 24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtggttg gggtttcttct tcctccctg 180

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acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360  
ttcaaaatac acaacgcgct aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420  
cacaacccag acaaggtgtg gtggggccaag aacagccagg ccaaaaccat tgccacggag 480  
tcttgctcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaa 600  
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgcagggaac 720  
cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780  
ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
ctcacacaaa tctaccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
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gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtacgtct aggggtgccc 1080  
aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
tggaacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagctt 1200  
gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
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accttggaag gatccttcac cagccccaat tacccaaagc cgcactctga gctggcttat 1500  
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
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aacttgcaac taaaagaccc aacttgacga ccaaaattat caaatgttgt ggaattttct 1920  
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
aatataatca ccttttctgc atcctcaact tctgaagtga tcacccgtca gaaacaactc 2040  
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
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gatacctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacaag 2340  
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gttttgatat gtgatagcag tgaccaccag tctcgctgca atcaagggtg tgtctccaga 2520  
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gaaactccaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700  
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

09902759.071001

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

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Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 565 |     | 570 |     | 575 |     |     |     |     |     |     |     |     |     |     |
| Leu | Ala | Leu | Asn | Val | Val | Thr | Val | Ala | Thr | Ile | Thr | Val | Arg | His | Phe |
|     | 580 |     |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Val | Asn | Gln | Arg | Ala | Asp | Tyr | Lys | Tyr | Gln | Lys | Leu | Gln | Asn | Tyr |     |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
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 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacactgg 180

FOOTNOTES 65220560

gagtccctgg acgcccgcga gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240  
 atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300  
 caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattacce tccagtttc 360  
 aaatatgaag attttgacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420  
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 tttacctgtt gggggtcaga atattcgtgg aactggaatg ccatagatga gggggccaaag 540  
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 ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660  
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 aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780  
 aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840  
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900  
 gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020  
 ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattggg 1080  
 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140  
 tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200  
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 cacaccta at gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980  
 actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040  
 gagaaggtac agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100  
 gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160  
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280  
 caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340  
 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

09902759.071001

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgcagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
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<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
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 gtgttgcttc tcaacttccat ctggaccacg aggtccctgg tccaaggctc ttgcggtgca 240  
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099029.0101  
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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                20                      25                      30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
                35                      40                      45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
  50                      55                      60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
  65                      70                      75                      80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
                85                      90                      95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
  100                      105                      110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
  115                      120                      125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
  130                      135                      140

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Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
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 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
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<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

0902259.01001

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

0990259.0301  
100720" 55/20650

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65              70              75              80

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F007206520660

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

&lt;210&gt; 208

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 cccattgctc ctgctgcccc gtcctacgg actgcccttc tacaacggct tctactactc 180  
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 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

09902759.07.1001

| 115   | 120 | 125 |
|---|-----|-----|
| Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr |     |     |
| 130   | 135 | 140 |
| Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu |     |     |
| 145   | 150 | 155 |
| Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg |     |     |
|   | 165 | 170 |
| Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala |     |     |
|   | 180 | 185 |
| Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly |     |     |
|   | 195 | 200 |
| Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr |     |     |
|   | 210 | 215 |
| Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro |     |     |
| 225   | 230 | 235 |
| Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp |     |     |
|   | 245 | 250 |
| Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu |     |     |
|   | 260 | 265 |
| His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu |     |     |
|   | 275 | 280 |
| Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys |     |     |
|   | 290 | 295 |
| Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser |     |     |
| 305   | 310 | 315 |
| Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu |     |     |
|   | 325 | 330 |
| Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr |     |     |
|   | 340 | 345 |
| Gly Val Tyr Cys Tyr Arg Gln His                                 |     |     |
|   | 355 | 360 |

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

FOOT-65220650



<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg ggttgagg 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtggag gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

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<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
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<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

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 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
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 <213> Homo sapiens

<400> 221  
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| 1   | 5   | 10  | 15  |
| Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly | 20  | 25  | 30  |
| Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala | 35  | 40  | 45  |
| His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val | 50  | 55  | 60  |
| Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu | 65  | 70  | 75  |
| Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp | 85  | 90  | 95  |
| Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg | 100 | 105 | 110 |
| His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp | 115 | 120 | 125 |
| Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly | 130 | 135 | 140 |
| His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr | 145 | 150 | 155 |
| Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp | 165 | 170 | 175 |
| Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu | 180 | 185 | 190 |
| His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr | 195 | 200 | 205 |
| Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu | 210 | 215 | 220 |
| Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala | 225 | 230 | 235 |
| Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn | 245 | 250 | 255 |
| Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro | 260 | 265 | 270 |
| Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu | 275 | 280 | 285 |

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Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
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Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
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Leu Thr Arg His His Asp Glu Leu  
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

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20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<400> 225  
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44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

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 atcctgggct tcgtcgtgatt tgccgcgcag ggcctccca gacctagagg ggcgtggcc 240  
 tggagcagcg ggtcgtctgt gtctctctct ctctgcgcgc cgcggggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctccgcacc ctggccttgc ccgcattctc 360  
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<210> 227

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 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

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Phe Leu Glu Ser Gln Gln  
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<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

FOOTNOTES



<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234

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45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
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 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                     100                    105                    110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                     115                    120                    125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                     130                    135                    140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                     145                    150                    155                    160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                     165                    170                    175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                     180                    185                    190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                     195                    200                    205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                     210                    215                    220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                     225                    230                    235                    240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                     245                    250                    255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                     260                    265                    270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                     275                    280                    285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                     290                    295                    300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                     305                    310                    315                    320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
                     325                    330                    335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
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<211> 17  
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 <223> Synthetic oligonucleotide probe

<400> 237  
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<210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 238  
 ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 239  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 239  
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<210> 240  
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<220>  
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<400> 240  
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<210> 241  
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<220>  
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<400> 241  
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<210> 242  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
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24

<210> 243  
 <211> 45  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
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45

<210> 244  
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 <212> DNA  
 <213> Homo Sapien

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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro  
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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
 65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
 80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His  
 125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
 140 145 150

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Leu | Tyr | Arg | Ile | Ala | Pro | Arg | Ala | Phe | Ser | Gly | Leu | Ser | 155 | 160 | 165 |
| Asn | Leu | Leu | Arg | Leu | His | Leu | Asn | Ser | Asn | Leu | Leu | Arg | Ala | Ile | 170 | 175 | 180 |
| Asp | Ser | Arg | Trp | Phe | Glu | Met | Leu | Pro | Asn | Leu | Glu | Ile | Leu | Met | 185 | 190 | 195 |
| Ile | Gly | Gly | Asn | Lys | Val | Asp | Ala | Ile | Leu | Asp | Met | Asn | Phe | Arg | 200 | 205 | 210 |
| Pro | Leu | Ala | Asn | Leu | Arg | Ser | Leu | Val | Leu | Ala | Gly | Met | Asn | Leu | 215 | 220 | 225 |
| Arg | Glu | Ile | Ser | Asp | Tyr | Ala | Leu | Glu | Gly | Leu | Gln | Ser | Leu | Glu | 230 | 235 | 240 |
| Ser | Leu | Ser | Phe | Tyr | Asp | Asn | Gln | Leu | Ala | Arg | Val | Pro | Arg | Arg | 245 | 250 | 255 |
| Ala | Leu | Glu | Gln | Val | Pro | Gly | Leu | Lys | Phe | Leu | Asp | Leu | Asn | Lys | 260 | 265 | 270 |
| Asn | Pro | Leu | Gln | Arg | Val | Gly | Pro | Gly | Asp | Phe | Ala | Asn | Met | Leu | 275 | 280 | 285 |
| His | Leu | Lys | Glu | Leu | Gly | Leu | Asn | Asn | Met | Glu | Glu | Leu | Val | Ser | 290 | 295 | 300 |
| Ile | Asp | Lys | Phe | Ala | Leu | Val | Asn | Leu | Pro | Glu | Leu | Thr | Lys | Leu | 305 | 310 | 315 |
| Asp | Ile | Thr | Asn | Asn | Pro | Arg | Leu | Ser | Phe | Ile | His | Pro | Arg | Ala | 320 | 325 | 330 |
| Phe | His | His | Leu | Pro | Gln | Met | Glu | Thr | Leu | Met | Leu | Asn | Asn | Asn | 335 | 340 | 345 |
| Ala | Leu | Ser | Ala | Leu | His | Gln | Gln | Thr | Val | Glu | Ser | Leu | Pro | Asn | 350 | 355 | 360 |
| Leu | Gln | Glu | Val | Gly | Leu | His | Gly | Asn | Pro | Ile | Arg | Cys | Asp | Cys | 365 | 370 | 375 |
| Val | Ile | Arg | Trp | Ala | Asn | Ala | Thr | Gly | Thr | Arg | Val | Arg | Phe | Ile | 380 | 385 | 390 |
| Glu | Pro | Gln | Ser | Thr | Leu | Cys | Ala | Glu | Pro | Pro | Asp | Leu | Gln | Arg | 395 | 400 | 405 |
| Leu | Pro | Val | Arg | Glu | Val | Pro | Phe | Arg | Glu | Met | Thr | Asp | His | Cys |     |     |     |

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|                                     |                         |     |
|-------------------------------------|-------------------------|-----|
| 410                                 | 415                     | 420 |
| Leu Pro Leu Ile Ser Pro Arg Ser Phe | Pro Pro Ser Leu Gln Val |     |
| 425                                 | 430                     | 435 |
| Ala Ser Gly Glu Ser Met Val Leu His | Cys Arg Ala Leu Ala Glu |     |
| 440                                 | 445                     | 450 |
| Pro Glu Pro Glu Ile Tyr Trp Val Thr | Pro Ala Gly Leu Arg Leu |     |
| 455                                 | 460                     | 465 |
| Thr Pro Ala His Ala Gly Arg Arg Tyr | Arg Val Tyr Pro Glu Gly |     |
| 470                                 | 475                     | 480 |
| Thr Leu Glu Leu Arg Arg Val Thr Ala | Glu Glu Ala Gly Leu Tyr |     |
| 485                                 | 490                     | 495 |
| Thr Cys Val Ala Gln Asn Leu Val Gly | Ala Asp Thr Lys Thr Val |     |
| 500                                 | 505                     | 510 |
| Ser Val Val Val Gly Arg Ala Leu Leu | Gln Pro Gly Arg Asp Glu |     |
| 515                                 | 520                     | 525 |
| Gly Gln Gly Leu Glu Leu Arg Val Gln | Glu Thr His Pro Tyr His |     |
| 530                                 | 535                     | 540 |
| Ile Leu Leu Ser Trp Val Thr Pro Pro | Asn Thr Val Ser Thr Asn |     |
| 545                                 | 550                     | 555 |
| Leu Thr Trp Ser Ser Ala Ser Ser Leu | Arg Gly Gln Gly Ala Thr |     |
| 560                                 | 565                     | 570 |
| Ala Leu Ala Arg Leu Pro Arg Gly Thr | His Ser Tyr Asn Ile Thr |     |
| 575                                 | 580                     | 585 |
| Arg Leu Leu Gln Ala Thr Glu Tyr Trp | Ala Cys Leu Gln Val Ala |     |
| 590                                 | 595                     | 600 |
| Phe Ala Asp Ala His Thr Gln Leu Ala | Cys Val Trp Ala Arg Thr |     |
| 605                                 | 610                     | 615 |
| Lys Glu Ala Thr Ser Cys His Arg Ala | Leu Gly Asp Arg Pro Gly |     |
| 620                                 | 625                     | 630 |
| Leu Ile Ala Ile Leu Ala Leu Ala Val | Leu Leu Leu Ala Ala Gly |     |
| 635                                 | 640                     | 645 |
| Leu Ala Ala His Leu Gly Thr Gly Gln | Pro Arg Lys Gly Val Gly |     |
| 650                                 | 655                     | 660 |
| Gly Arg Arg Pro Leu Pro Pro Ala Trp | Ala Phe Trp Gly Trp Ser |     |
| 665                                 | 670                     | 675 |

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Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                                 695                                700                                705

Leu Pro Pro Leu Ser Gln Asn Ser  
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgtag atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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090259-01001

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 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Arg | Gln | Thr | Ile | Ile | Lys | Val | Ile | Lys | Phe | Ile | Leu | Ile | Ile | 1  | 5  | 10 | 15 |
| Cys | Tyr | Thr | Val | Tyr | Tyr | Val | His | Asn | Ile | Lys | Phe | Asp | Val | Asp | 20 | 25 | 30 |    |
| Cys | Thr | Val | Asp | Ile | Glu | Ser | Leu | Thr | Gly | Tyr | Arg | Thr | Tyr | Arg | 35 | 40 | 45 |    |
| Cys | Ala | His | Pro | Leu | Ala | Thr | Leu | Phe | Lys | Ile | Leu | Ala | Ser | Phe | 50 | 55 | 60 |    |
| Tyr | Ile | Ser | Leu | Val | Ile | Phe | Tyr | Gly | Leu | Ile | Cys | Met | Tyr | Thr | 65 | 70 | 75 |    |
| Leu | Trp | Trp | Met | Leu | Arg | Arg | Ser | Leu | Lys | Lys | Tyr | Ser | Phe | Glu | 80 | 85 | 90 |    |
| Ser | Ile | Arg | Glu | Glu | Ser | Ser | Tyr | Ser | Asp | Ile | Pro | Asp | Val | Lys |    |    |    |    |

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|                 |                     |                     |     |  |     |
|-----------------|---------------------|---------------------|-----|--|-----|
|                 | 95                  |                     | 100 |  | 105 |
| Asn Asp Phe Ala | Phe Met Leu His Leu | Ile Asp Gln Tyr Asp | Pro |  |     |
|                 | 110                 |                     | 115 |  | 120 |
| Leu Tyr Ser Lys | Arg Phe Ala Val Phe | Leu Ser Glu Val Ser | Glu |  |     |
|                 | 125                 |                     | 130 |  | 135 |
| Asn Lys Leu Arg | Gln Leu Asn Leu Asn | Asn Glu Trp Thr Leu | Asp |  |     |
|                 | 140                 |                     | 145 |  | 150 |
| Lys Leu Arg Gln | Arg Leu Thr Lys Asn | Ala Gln Asp Lys Leu | Glu |  |     |
|                 | 155                 |                     | 160 |  | 165 |
| Leu His Leu Phe | Met Leu Ser Gly Ile | Pro Asp Thr Val Phe | Asp |  |     |
|                 | 170                 |                     | 175 |  | 180 |
| Leu Val Glu Leu | Glu Val Leu Lys Leu | Glu Leu Ile Pro Asp | Val |  |     |
|                 | 185                 |                     | 190 |  | 195 |
| Thr Ile Pro Pro | Ser Ile Ala Gln Leu | Thr Gly Leu Lys Glu | Leu |  |     |
|                 | 200                 |                     | 205 |  | 210 |
| Trp Leu Tyr His | Thr Ala Ala Lys Ile | Glu Ala Pro Ala Leu | Ala |  |     |
|                 | 215                 |                     | 220 |  | 225 |
| Phe Leu Arg Glu | Asn Leu Arg Ala Leu | His Ile Lys Phe Thr | Asp |  |     |
|                 | 230                 |                     | 235 |  | 240 |
| Ile Lys Glu Ile | Pro Leu Trp Ile Tyr | Ser Leu Lys Thr Leu | Glu |  |     |
|                 | 245                 |                     | 250 |  | 255 |
| Glu Leu His Leu | Thr Gly Asn Leu Ser | Ala Glu Asn Asn Arg | Tyr |  |     |
|                 | 260                 |                     | 265 |  | 270 |
| Ile Val Ile Asp | Gly Leu Arg Glu Leu | Lys Arg Leu Lys Val | Leu |  |     |
|                 | 275                 |                     | 280 |  | 285 |
| Arg Leu Lys Ser | Asn Leu Ser Lys Leu | Pro Gln Val Val Thr | Asp |  |     |
|                 | 290                 |                     | 295 |  | 300 |
| Val Gly Val His | Leu Gln Lys Leu Ser | Ile Asn Asn Glu Gly | Thr |  |     |
|                 | 305                 |                     | 310 |  | 315 |
| Lys Leu Ile Val | Leu Asn Ser Leu Lys | Lys Met Ala Asn Leu | Thr |  |     |
|                 | 320                 |                     | 325 |  | 330 |
| Glu Leu Glu Leu | Ile Arg Cys Asp Leu | Glu Arg Ile Pro His | Ser |  |     |
|                 | 335                 |                     | 340 |  | 345 |
| Ile Phe Ser Leu | His Asn Leu Gln Glu | Ile Asp Leu Lys Asp | Asn |  |     |
|                 | 350                 |                     | 355 |  | 360 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Lys | Thr | Ile | Glu | Glu | Ile | Ile | Ser | Phe | Gln | His | Leu | His |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |
| Arg | Leu | Thr | Cys | Leu | Lys | Leu | Trp | Tyr | Asn | His | Ile | Ala | Tyr | Ile |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |
| Pro | Ile | Gln | Ile | Gly | Asn | Leu | Thr | Asn | Leu | Glu | Arg | Leu | Tyr | Leu |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |
| Asn | Arg | Asn | Lys | Ile | Glu | Lys | Ile | Pro | Thr | Gln | Leu | Phe | Tyr | Cys |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |
| Arg | Lys | Leu | Arg | Tyr | Leu | Asp | Leu | Ser | His | Asn | Asn | Leu | Thr | Phe |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |
| Leu | Pro | Ala | Asp | Ile | Gly | Leu | Leu | Gln | Asn | Leu | Gln | Asn | Leu | Ala |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |
| Ile | Thr | Ala | Asn | Arg | Ile | Glu | Thr | Leu | Pro | Pro | Glu | Leu | Phe | Gln |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |
| Cys | Arg | Lys | Leu | Arg | Ala | Leu | His | Leu | Gly | Asn | Asn | Val | Leu | Gln |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Leu | Pro | Ser | Arg | Val | Gly | Glu | Leu | Thr | Asn | Leu | Thr | Gln | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |
| Glu | Leu | Arg | Gly | Asn | Arg | Leu | Glu | Cys | Leu | Pro | Val | Glu | Leu | Gly |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |
| Glu | Cys | Pro | Leu | Leu | Lys | Arg | Ser | Gly | Leu | Val | Val | Glu | Glu | Asp |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |
| Leu | Phe | Asn | Thr | Leu | Pro | Pro | Glu | Val | Lys | Glu | Arg | Leu | Trp | Arg |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |
| Ala | Asp | Lys | Glu | Gln | Ala |     |     |     |     |     |     |     |     |     |
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&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

09902759.071001



<212> DNA

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<210> 253

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<213> Artificial Sequence

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<213> Homo Sapien

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<211> 452

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<213> Homo Sapien

<400> 255

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| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn | 50  | 55  | 60  |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln | 65  | 70  | 75  |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu | 80  | 85  | 90  |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp | 95  | 100 | 105 |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr | 110 | 115 | 120 |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu | 125 | 130 | 135 |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe | 140 | 145 | 150 |
| Ser | Cys | His | Lys | Glu | Phe | Gln | Thr | Val | Pro | Phe | Tyr | Ile | Phe | Ser | 155 | 160 | 165 |
| Glu | Ser | Tyr | Gly | Gly | Lys | Met | Ala | Ala | Gly | Ile | Gly | Leu | Glu | Leu | 170 | 175 | 180 |
| Tyr | Lys | Ala | Ile | Gln | Arg | Gly | Thr | Ile | Lys | Cys | Asn | Phe | Ala | Gly | 185 | 190 | 195 |
| Val | Ala | Leu | Gly | Asp | Ser | Trp | Ile | Ser | Pro | Val | Asp | Ser | Val | Leu | 200 | 205 | 210 |
| Ser | Trp | Gly | Pro | Tyr | Leu | Tyr | Ser | Met | Ser | Leu | Leu | Glu | Asp | Lys | 215 | 220 | 225 |
| Gly | Leu | Ala | Glu | Val | Ser | Lys | Val | Ala | Glu | Gln | Val | Leu | Asn | Ala | 230 | 235 | 240 |
| Val | Asn | Lys | Gly | Leu | Tyr | Arg | Glu | Ala | Thr | Glu | Leu | Trp | Gly | Lys | 245 | 250 | 255 |
| Ala | Glu | Met | Ile | Ile | Glu | Gln | Asn | Thr | Asp | Gly | Val | Asn | Phe | Tyr | 260 | 265 | 270 |
| Asn | Ile | Leu | Thr | Lys | Ser | Thr | Pro | Thr | Ser | Thr | Met | Glu | Ser | Ser | 275 | 280 | 285 |
| Leu | Glu | Phe | Thr | Gln | Ser | His | Leu | Val | Cys | Leu | Cys | Gln | Arg | His | 290 | 295 | 300 |
| Val | Arg | His | Leu | Gln | Arg | Asp | Ala | Leu | Ser | Gln | Leu | Met | Asn | Gly |     |     |     |

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|                 |                     |                         |     |  |     |
|-----------------|---------------------|-------------------------|-----|--|-----|
|                 | 305                 |                         | 310 |  | 315 |
| Pro Ile Arg Lys | Lys Leu Lys Ile Ile | Pro Glu Asp Gln Ser Trp |     |  |     |
|                 | 320                 | 325                     |     |  | 330 |
| Gly Gly Gln Ala | Thr Asn Val Phe Val | Asn Met Glu Glu Asp Phe |     |  |     |
|                 | 335                 | 340                     |     |  | 345 |
| Met Lys Pro Val | Ile Ser Ile Val Asp | Glu Leu Leu Glu Ala Gly |     |  |     |
|                 | 350                 | 355                     |     |  | 360 |
| Ile Asn Val Thr | Val Tyr Asn Gly Gln | Leu Asp Leu Ile Val Asp |     |  |     |
|                 | 365                 | 370                     |     |  | 375 |
| Thr Met Gly Gln | Glu Ala Trp Val Arg | Lys Leu Lys Trp Pro Glu |     |  |     |
|                 | 380                 | 385                     |     |  | 390 |
| Leu Pro Lys Phe | Ser Gln Leu Lys Trp | Lys Ala Leu Tyr Ser Asp |     |  |     |
|                 | 395                 | 400                     |     |  | 405 |
| Pro Lys Ser Leu | Glu Thr Ser Ala Phe | Val Lys Ser Tyr Lys Asn |     |  |     |
|                 | 410                 | 415                     |     |  | 420 |
| Leu Ala Phe Tyr | Trp Ile Leu Lys Ala | Gly His Met Val Pro Ser |     |  |     |
|                 | 425                 | 430                     |     |  | 435 |
| Asp Gln Gly Asp | Met Ala Leu Lys Met | Met Arg Leu Val Thr Gln |     |  |     |
|                 | 440                 | 445                     |     |  | 450 |

Gln Glu

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<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgccca tccttctgga 350
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<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Arg | Gly | Ala | Leu | Leu | Leu | Ala | Leu | Leu | Leu | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Leu | Arg | Lys | Pro | Glu | Ser | Gln | Glu | Ala | Ala | Pro | Leu | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Cys | Gly | Arg | Arg | Val | Ile | Thr | Ser | Arg | Ile | Val | Gly | Gly |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ala | Glu | Leu | Gly | Arg | Trp | Pro | Trp | Gln | Gly | Ser | Leu | Arg |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Asp | Ser | His | Val | Cys | Gly | Val | Ser | Leu | Leu | Ser | His | Arg |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Leu | Thr | Ala | Ala | His | Cys | Phe | Glu | Thr | Tyr | Ser | Asp | Leu |
|     |     |     | 80  |     |     |     |     |     | 85  |     |     |     | 90  |     |

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Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
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 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
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 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
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 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
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 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
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 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
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 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
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&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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| Met | Gly | Leu | Gln | Ala | Cys | Leu | Leu | Gly | Leu | Phe | Ala | Leu | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

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|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 20  |  | 25  |  | 30  |
| Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu | 35  |  | 40  |  | 45  |
| Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg | 50  |  | 55  |  | 60  |
| Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln | 65  |  | 70  |  | 75  |
| Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg | 80  |  | 85  |  | 90  |
| Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala | 95  |  | 100 |  | 105 |
| Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu | 110 |  | 115 |  | 120 |
| Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly | 125 |  | 130 |  | 135 |
| Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val | 140 |  | 145 |  | 150 |
| Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro | 155 |  | 160 |  | 165 |
| His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser | 170 |  | 175 |  | 180 |
| Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly | 185 |  | 190 |  | 195 |
| Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn | 200 |  | 205 |  | 210 |
| Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln | 215 |  | 220 |  | 225 |
| Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu | 230 |  | 235 |  | 240 |
| Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala | 245 |  | 250 |  | 255 |
| Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly | 260 |  | 265 |  | 270 |
| Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala | 275 |  | 280 |  | 285 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ile | Ser | Thr | Trp | Val | Tyr | Ser | Ser | Pro | Gly | Arg | His | Glu | Gly |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Gln | Glu | Pro | Phe | Leu | Gln | Trp | Leu | Met | Leu | Leu | Ser | Asn | Glu | Ser |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |  |
| Ala | Leu | Pro | His | Val | His | Thr | Val | Ser | Tyr | Gly | Asp | Asp | Glu | Asp |  |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |  |
| Ser | Leu | Ser | Ser | Ala | Tyr | Ile | Gln | Arg | Val | Asn | Thr | Glu | Leu | Met |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |  |
| Lys | Ala | Ala | Ala | Arg | Gly | Leu | Thr | Leu | Leu | Phe | Ala | Ser | Gly | Asp |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |  |
| Ser | Gly | Ala | Gly | Cys | Trp | Ser | Val | Ser | Gly | Arg | His | Gln | Phe | Arg |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |  |
| Pro | Thr | Phe | Pro | Ala | Ser | Ser | Pro | Tyr | Val | Thr | Thr | Val | Gly | Gly |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |  |
| Thr | Ser | Phe | Gln | Glu | Pro | Phe | Leu | Ile | Thr | Asn | Glu | Ile | Val | Asp |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |  |
| Tyr | Ile | Ser | Gly | Gly | Gly | Phe | Ser | Asn | Val | Phe | Pro | Arg | Pro | Ser |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |  |
| Tyr | Gln | Glu | Glu | Ala | Val | Thr | Lys | Phe | Leu | Ser | Ser | Ser | Pro | His |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |  |
| Leu | Pro | Pro | Ser | Ser | Tyr | Phe | Asn | Ala | Ser | Gly | Arg | Ala | Tyr | Pro |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |  |
| Asp | Val | Ala | Ala | Leu | Ser | Asp | Gly | Tyr | Trp | Val | Val | Ser | Asn | Arg |  |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |  |
| Val | Pro | Ile | Pro | Trp | Val | Ser | Gly | Thr | Ser | Ala | Ser | Thr | Pro | Val |  |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Phe | Gly | Gly | Ile | Leu | Ser | Leu | Ile | Asn | Glu | His | Arg | Ile | Leu | Ser |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |  |
| Gly | Arg | Pro | Pro | Leu | Gly | Phe | Leu | Asn | Pro | Arg | Leu | Tyr | Gln | Gln |  |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |  |
| His | Gly | Ala | Gly | Leu | Phe | Asp | Val | Thr | Arg | Gly | Cys | His | Glu | Ser |  |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |  |
| Cys | Leu | Asp | Glu | Glu | Val | Glu | Gly | Gln | Gly | Phe | Cys | Ser | Gly | Pro |  |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |  |
| Gly | Trp | Asp | Pro | Val | Thr | Gly | Trp | Gly | Thr | Pro | Thr | Ser | Gln | Leu |  |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |  |

09902759.071001

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ile | Pro | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Trp | Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Leu | Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Ser | Ser | Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Tyr | Glu | Glu | Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Asn | Gly | Ser | Arg | Thr | Glu | Thr | Gln | Val | Gly | Ile | Tyr | Ile |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Ser | Gly | Asp | Gly | Ala | Gln | His | Arg | Asp | Ser | Gly | Ser |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |

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|                 |   |     |     |     |
|-----------------|---|-----|-----|-----|
| Ser Gly Lys Ser | Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser | 125 | 130 | 135 |
| Arg Phe Ser Ile | Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe | 140 | 145 | 150 |
| Ser Thr Ser Val | Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val | 155 | 160 | 165 |
| Ala Glu Lys His | Val Leu Thr Ala Ala His Cys Ile His Asp Gly | 170 | 175 | 180 |
| Lys Thr Tyr Val | Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu | 185 | 190 | 195 |
| Lys Pro Lys Phe | Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr | 200 | 205 | 210 |
| Ser Ala Met Pro | Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys | 215 | 220 | 225 |
| Arg Thr His Val | Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp | 230 | 235 | 240 |
| Ile Gly Met Asp | Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro | 245 | 250 | 255 |
| His Lys Arg Lys | Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys | 260 | 265 | 270 |
| Gln Leu Pro Gly | Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp | 275 | 280 | 285 |
| Arg Pro Gly Asn | Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu | 290 | 295 | 300 |
| Thr Tyr Asp Leu | Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala | 305 | 310 | 315 |
| Ser Gly Ser Gly | Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln | 320 | 325 | 330 |
| Lys Trp Glu Arg | Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp | 335 | 340 | 345 |
| Val Asp Met Asn | Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg | 350 | 355 | 360 |
| Ile Thr Pro Leu | Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly | 365 | 370 | 375 |
| Asn Tyr Leu Asp | Cys Arg Glu Gly                             | 380 |     |     |

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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien.

<400> 263

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Val | Ser | Gly | Ala | Pro | Pro | Ala | Leu | Gly | Gly | Gly | Cys | Leu | 1   | 5   | 10  | 15 |
| Gly | Thr | Phe | Thr | Ser | Leu | Leu | Leu | Leu | Ala | Ser | Thr | Ala | Ile | Leu | 20  | 25  | 30  |    |
| Asn | Ala | Ala | Arg | Ile | Pro | Val | Pro | Pro | Ala | Cys | Gly | Lys | Pro | Gln | 35  | 40  | 45  |    |
| Gln | Leu | Asn | Arg | Val | Val | Gly | Gly | Glu | Asp | Ser | Thr | Asp | Ser | Glu | 50  | 55  | 60  |    |
| Trp | Pro | Trp | Ile | Val | Ser | Ile | Gln | Lys | Asn | Gly | Thr | His | His | Cys | 65  | 70  | 75  |    |
| Ala | Gly | Ser | Leu | Leu | Thr | Ser | Arg | Trp | Val | Ile | Thr | Ala | Ala | His | 80  | 85  | 90  |    |
| Cys | Phe | Lys | Asp | Asn | Leu | Asn | Lys | Pro | Tyr | Leu | Phe | Ser | Val | Leu | 95  | 100 | 105 |    |
| Leu | Gly | Ala | Trp | Gln | Leu | Gly | Asn | Pro | Gly | Ser | Arg | Ser | Gln | Lys | 110 | 115 | 120 |    |
| Val | Gly | Val | Ala | Trp | Val | Glu | Pro | His | Pro | Val | Tyr | Ser | Trp | Lys | 125 | 130 | 135 |    |
| Glu | Gly | Ala | Cys | Ala | Asp | Ile | Ala | Leu | Val | Arg | Leu | Glu | Arg | Ser | 140 | 145 | 150 |    |
| Ile | Gln | Phe | Ser | Glu | Arg | Val | Leu | Pro | Ile | Cys | Leu | Pro | Asp | Ala | 155 | 160 | 165 |    |
| Ser | Ile | His | Leu | Pro | Pro | Asn | Thr | His | Cys | Trp | Ile | Ser | Gly | Trp | 170 | 175 | 180 |    |

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|   |                         |
|---|-------------------------|
| Gly Ser Ile Gln Asp Gly Val Pro Leu                         | Pro His Pro Gln Thr Leu |
| 185   | 190 195                 |
| Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His |                         |
| 200   | 205 210                 |
| Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met |                         |
| 215   | 220 225                 |
| Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly |                         |
| 230   | 235 240                 |
| Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu |                         |
| 245   | 250 255                 |
| Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn |                         |
| 260   | 265 270                 |
| Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val |                         |
| 275   | 280 285                 |
| Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly |                         |
| 290   | 295 300                 |
| Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala |                         |
| 305   | 310 315                 |

Arg Ser

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

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<210> 266

<211> 24

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<212> DNA  
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<223> Synthetic Oligonucleotide Probe

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<210> 271  
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<210> 272  
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<220>  
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<400> 272  
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<210> 273  
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<210> 274  
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<223> Synthetic Oligonucleotide Probe

<400> 280

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<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 281

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<220>

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<210> 283

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<213> Artificial Sequence

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<211> 1875

<212> DNA

<213> Homo Sapien

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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Gly | Ser | Cys | Ser | Phe | Leu | Met | Leu | Leu | Leu | Pro | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Val | Ala | Thr | Thr | Gly | Pro | Val | Gly | Ala | Leu | Thr | Asp |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Lys | Arg | Leu | Met | Val | Glu | Leu | His | Asn | Leu | Tyr | Arg | Ala |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Ser | Pro | Thr | Ala | Ser | Asp | Met | Leu | His | Met | Arg | Trp | Asp |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Leu | Ala | Ala | Phe | Ala | Lys | Ala | Tyr | Ala | Arg | Gln | Cys | Val |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Gly | His | Asn | Lys | Glu | Arg | Gly | Arg | Arg | Gly | Glu | Asn | Leu | Phe |
|     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Thr | Asp | Glu | Gly | Met | Asp | Val | Pro | Leu | Ala | Met | Glu | Glu |
|     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |     | 105 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | His | His | Glu | Arg | Glu | His | Tyr | Asn | Leu | Ser | Ala | Ala | Thr | Cys |
|     |     |     | 110 |     |     |     |     |     | 115 |     |     |     |     | 120 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Gly | Gln | Met | Cys | Gly | His | Tyr | Thr | Gln | Val | Val | Trp | Ala |
|     |     |     | 125 |     |     |     |     |     | 130 |     |     |     |     | 135 |

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|                 |   |     |     |     |
|-----------------|---|-----|-----|-----|
| Lys Thr Glu Arg | Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu | 140 | 145 | 150 |
| Gln Gly Val Glu | Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr | 155 | 160 | 165 |
| Glu Pro Pro Gly | Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly | 170 | 175 | 180 |
| Thr Pro Cys Ser | Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser | 185 | 190 | 195 |
| Leu Cys Glu Pro | Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro | 200 | 205 | 210 |
| Tyr Leu Val Thr | Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser | 215 | 220 | 225 |
| Asp Ser Arg Lys | Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile | 230 | 235 | 240 |
| Pro Ala Phe Leu | Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys | 245 | 250 | 255 |
| Ala Leu Pro Ala | Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr | 260 | 265 | 270 |
| Lys Asp Pro Pro | Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr | 275 | 280 | 285 |
| Thr Glu Val Pro | Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu | 290 | 295 | 300 |
| Asp Glu Glu Pro | Val Thr Phe Pro Lys Ser Thr His Val Pro Ile | 305 | 310 | 315 |
| Pro Lys Ser Ala | Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser | 320 | 325 | 330 |
| Arg Ser Pro Glu | Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly | 335 | 340 | 345 |
| Ala Arg Glu Leu | Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu | 350 | 355 | 360 |
| Ala Glu Leu Pro | Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro | 365 | 370 | 375 |
| Ala Gln Asp Lys | Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr | 380 | 385 | 390 |
| Gly His Thr Ser | Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser | 395 | 400 | 405 |

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Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
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<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Val | Leu | Leu | Leu | Phe | Ser | Leu | Cys | Leu | Leu | Phe | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Pro | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Ser | Met | Ser | His | Leu | Gln | Ser | Leu | Arg | Glu | Val | Lys | Leu | 35  | 40  | 45  |
| Asn | Asn | Asn | Glu | Leu | Glu | Thr | Ile | Pro | Asn | Leu | Gly | Pro | Val | Ser | 50  | 55  | 60  |
| Ala | Asn | Ile | Thr | Leu | Leu | Ser | Leu | Ala | Gly | Asn | Arg | Ile | Val | Glu | 65  | 70  | 75  |
| Ile | Leu | Pro | Glu | His | Leu | Lys | Glu | Phe | Gln | Ser | Leu | Glu | Thr | Leu | 80  | 85  | 90  |
| Asp | Leu | Ser | Ser | Asn | Asn | Ile | Ser | Glu | Leu | Gln | Thr | Ala | Phe | Pro | 95  | 100 | 105 |
| Ala | Leu | Gln | Leu | Lys | Tyr | Leu | Tyr | Leu | Asn | Ser | Asn | Arg | Val | Thr | 110 | 115 | 120 |
| Ser | Met | Glu | Pro | Gly | Tyr | Phe | Asp | Asn | Leu | Ala | Asn | Thr | Leu | Leu | 125 | 130 | 135 |
| Val | Leu | Lys | Leu | Asn | Arg | Asn | Arg | Ile | Ser | Ala | Ile | Pro | Pro | Lys | 140 | 145 | 150 |
| Met | Phe | Lys | Leu | Pro | Gln | Leu | Gln | His | Leu | Glu | Leu | Asn | Arg | Asn | 155 | 160 | 165 |
| Lys | Ile | Lys | Asn | Val | Asp | Gly | Leu | Thr | Phe | Gln | Gly | Leu | Gly | Ala | 170 | 175 | 180 |
| Leu | Lys | Ser | Leu | Lys | Met | Gln | Arg | Asn | Gly | Val | Thr | Lys | Leu | Met | 185 | 190 | 195 |
| Asp | Gly | Ala | Phe | Trp | Gly | Leu | Ser | Asn | Met | Glu | Ile | Leu | Gln | Leu | 200 | 205 | 210 |
| Asp | His | Asn | Asn | Leu | Thr | Glu | Ile | Thr | Lys | Gly | Trp | Leu | Tyr | Gly | 215 | 220 | 225 |
| Leu | Leu | Met | Leu | Gln | Glu | Leu | His | Leu | Ser | Gln | Asn | Ala | Ile | Asn | 230 | 235 | 240 |
| Arg | Ile | Ser | Pro | Asp | Ala | Trp | Glu | Phe | Cys | Gln | Lys | Leu | Ser | Glu | 245 | 250 | 255 |
| Leu | Asp | Leu | Thr | Phe | Asn | His | Leu | Ser | Arg | Leu | Asp | Asp | Ser | Ser | 260 | 265 | 270 |
| Phe | Leu | Gly | Leu | Ser | Leu | Leu | Asn | Thr | Leu | His | Ile | Gly | Asn | Asn | 275 | 280 | 285 |
| Arg | Val | Ser | Tyr | Ile | Ala | Asp | Cys | Ala | Phe | Arg | Gly | Leu | Ser | Ser |     |     |     |

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| 290 |     |     |     |     |     |     |     |     |     | 295 |     |     |     |     | 300 |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Leu | Lys | Thr | Leu | Asp | Leu | Lys | Asn | Asn | Glu | Ile | Ser | Trp | Thr | Ile |     |  |  |  |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |  |  |  |  |
| Glu | Asp | Met | Asn | Gly | Ala | Phe | Ser | Gly | Leu | Asp | Lys | Leu | Arg | Arg |     |  |  |  |  |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |  |  |  |  |
| Leu | Ile | Leu | Gln | Gly | Asn | Arg | Ile | Arg | Ser | Ile | Thr | Lys | Lys | Ala |     |  |  |  |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |  |  |  |  |
| Phe | Thr | Gly | Leu | Asp | Ala | Leu | Glu | His | Leu | Asp | Leu | Ser | Asp | Asn |     |  |  |  |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |     |  |  |  |  |
| Ala | Ile | Met | Ser | Leu | Gln | Gly | Asn | Ala | Phe | Ser | Gln | Met | Lys | Lys |     |  |  |  |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |     |  |  |  |  |
| Leu | Gln | Gln | Leu | His | Leu | Asn | Thr | Ser | Ser | Leu | Leu | Cys | Asp | Cys |     |  |  |  |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |     |  |  |  |  |
| Gln | Leu | Lys | Trp | Leu | Pro | Gln | Trp | Val | Ala | Glu | Asn | Asn | Phe | Gln |     |  |  |  |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |     |  |  |  |  |
| Ser | Phe | Val | Asn | Ala | Ser | Cys | Ala | His | Pro | Gln | Leu | Leu | Lys | Gly |     |  |  |  |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |     |  |  |  |  |
| Arg | Ser | Ile | Phe | Ala | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp |     |  |  |  |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |     |  |  |  |  |
| Phe | Pro | Lys | Pro | Gln | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala |     |  |  |  |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |     |  |  |  |  |
| Ile | Lys | Gly | Ser | Asn | Leu | Ser | Phe | Ile | Cys | Ser | Ala | Ala | Ser | Ser |     |  |  |  |  |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |     |  |  |  |  |
| Ser | Asp | Ser | Pro | Met | Thr | Phe | Ala | Trp | Lys | Lys | Asp | Asn | Glu | Leu |     |  |  |  |  |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |     |  |  |  |  |
| Leu | His | Asp | Ala | Glu | Met | Glu | Asn | Tyr | Ala | His | Leu | Arg | Ala | Gln |     |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |
| Gly | Gly | Glu | Val | Met | Glu | Tyr | Thr | Thr | Ile | Leu | Arg | Leu | Arg | Glu |     |  |  |  |  |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |  |  |  |  |
| Val | Glu | Phe | Ala | Ser | Glu | Gly | Lys | Tyr | Gln | Cys | Val | Ile | Ser | Asn |     |  |  |  |  |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |  |  |  |  |
| His | Phe | Gly | Ser | Ser | Tyr | Ser | Val | Lys | Ala | Lys | Leu | Thr | Val | Asn |     |  |  |  |  |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |  |  |  |  |
| Met | Leu | Pro | Ser | Phe | Thr | Lys | Thr | Pro | Met | Asp | Leu | Thr | Ile | Arg |     |  |  |  |  |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |  |  |  |  |

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|                 |                     |                     |     |
|-----------------|---------------------|---------------------|-----|
| Ala Gly Ala Met | Ala Arg Leu Glu Cys | Ala Ala Val Gly His | Pro |
| 560             |                     | 565                 | 570 |
| Ala Pro Gln Ile | Ala Trp Gln Lys Asp | Gly Gly Thr Asp Phe | Pro |
| 575             |                     | 580                 | 585 |
| Ala Ala Arg Glu | Arg Arg Met His Val | Met Pro Glu Asp Asp | Val |
| 590             |                     | 595                 | 600 |
| Phe Phe Ile Val | Asp Val Lys Ile Glu | Asp Ile Gly Val Tyr | Ser |
| 605             |                     | 610                 | 615 |
| Cys Thr Ala Gln | Asn Ser Ala Gly Ser | Ile Ser Ala Asn Ala | Thr |
| 620             |                     | 625                 | 630 |
| Leu Thr Val Leu | Glu Thr Pro Ser Phe | Leu Arg Pro Leu Leu | Asp |
| 635             |                     | 640                 | 645 |
| Arg Thr Val Thr | Lys Gly Glu Thr Ala | Val Leu Gln Cys Ile | Ala |
| 650             |                     | 655                 | 660 |
| Gly Gly Ser Pro | Pro Pro Lys Leu Asn | Trp Thr Lys Asp Asp | Ser |
| 665             |                     | 670                 | 675 |
| Pro Leu Val Val | Thr Glu Arg His Phe | Phe Ala Ala Gly Asn | Gln |
| 680             |                     | 685                 | 690 |
| Leu Leu Ile Ile | Val Asp Ser Asp Val | Ser Asp Ala Gly Lys | Tyr |
| 695             |                     | 700                 | 705 |
| Thr Cys Glu Met | Ser Asn Thr Leu Gly | Thr Glu Arg Gly Asn | Val |
| 710             |                     | 715                 | 720 |
| Arg Leu Ser Val | Ile Pro Thr Pro Thr | Cys Asp Ser Pro Gln | Met |
| 725             |                     | 730                 | 735 |
| Thr Ala Pro Ser | Leu Asp Asp Asp Gly | Trp Ala Thr Val Gly | Val |
| 740             |                     | 745                 | 750 |
| Val Ile Ile Ala | Val Val Cys Cys Val | Val Gly Thr Ser Leu | Val |
| 755             |                     | 760                 | 765 |
| Trp Val Val Ile | Ile Tyr His Thr Arg | Arg Arg Asn Glu Asp | Cys |
| 770             |                     | 775                 | 780 |
| Ser Ile Thr Asn | Thr Asp Glu Thr Asn | Leu Pro Ala Asp Ile | Pro |
| 785             |                     | 790                 | 795 |
| Ser Tyr Leu Ser | Ser Gln Gly Thr Leu | Ala Asp Arg Gln Asp | Gly |
| 800             |                     | 805                 | 810 |

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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
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&lt;211&gt; 2906

FOOT 20" 65220560

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Leu | Asn | Lys | Met | Thr | Leu | His | Pro | Gln | Gln | Ile | Met | Ile | Gly | 1   | 5   | 10  | 15 |
| Pro | Arg | Phe | Asn | Arg | Ala | Leu | Phe | Asp | Pro | Leu | Leu | Val | Val | Leu | 20  | 25  | 30  |    |
| Leu | Ala | Leu | Gln | Leu | Leu | Val | Val | Ala | Gly | Leu | Val | Arg | Ala | Gln | 35  | 40  | 45  |    |
| Thr | Cys | Pro | Ser | Val | Cys | Ser | Cys | Ser | Asn | Gln | Phe | Ser | Lys | Val | 50  | 55  | 60  |    |
| Ile | Cys | Val | Arg | Lys | Asn | Leu | Arg | Glu | Val | Pro | Asp | Gly | Ile | Ser | 65  | 70  | 75  |    |
| Thr | Asn | Thr | Arg | Leu | Leu | Asn | Leu | His | Glu | Asn | Gln | Ile | Gln | Ile | 80  | 85  | 90  |    |
| Ile | Lys | Val | Asn | Ser | Phe | Lys | His | Leu | Arg | His | Leu | Glu | Ile | Leu | 95  | 100 | 105 |    |
| Gln | Leu | Ser | Arg | Asn | His | Ile | Arg | Thr | Ile | Glu | Ile | Gly | Ala | Phe | 110 | 115 | 120 |    |
| Asn | Gly | Leu | Ala | Asn | Leu | Asn | Thr | Leu | Glu | Leu | Phe | Asp | Asn | Arg | 125 | 130 | 135 |    |
| Leu | Thr | Thr | Ile | Pro | Asn | Gly | Ala | Phe | Val | Tyr | Leu | Ser | Lys | Leu | 140 | 145 | 150 |    |
| Lys | Glu | Leu | Trp | Leu | Arg | Asn | Asn | Pro | Ile | Glu | Ser | Ile | Pro | Ser |     |     |     |    |

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| Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly | 185 |  | 190 |  | 195 |
| Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg | 200 |  | 205 |  | 210 |
| Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp | 215 |  | 220 |  | 225 |
| Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln | 230 |  | 235 |  | 240 |
| Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile | 245 |  | 250 |  | 255 |
| Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val | 260 |  | 265 |  | 270 |
| Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp | 275 |  | 280 |  | 285 |
| Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His | 290 |  | 295 |  | 300 |
| Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp | 305 |  | 310 |  | 315 |
| Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys | 320 |  | 325 |  | 330 |
| Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp | 335 |  | 340 |  | 345 |
| Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro | 350 |  | 355 |  | 360 |
| Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys | 365 |  | 370 |  | 375 |
| Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn | 380 |  | 385 |  | 390 |
| Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val | 395 |  | 400 |  | 405 |
| Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp | 410 |  | 415 |  | 420 |

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 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
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&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

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| 230   | 235                     | 240 |     |  |     |
| Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met |                         |     |     |  |     |
| 245   | 250                     | 255 |     |  |     |
| Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu |                         |     |     |  |     |
| 260   | 265                     | 270 |     |  |     |
| Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly |                         |     |     |  |     |
| 275   | 280                     | 285 |     |  |     |
| Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn |                         |     |     |  |     |
| 290   | 295                     | 300 |     |  |     |
| Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu |                         |     |     |  |     |
| 305   | 310                     | 315 |     |  |     |
| Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser |                         |     |     |  |     |
| 320   | 325                     | 330 |     |  |     |
| Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn |                         |     |     |  |     |
| 335   | 340                     | 345 |     |  |     |
| Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser |                         |     |     |  |     |
| 350   | 355                     | 360 |     |  |     |
| Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile |                         |     |     |  |     |
| 365   | 370                     | 375 |     |  |     |
| Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg |                         |     |     |  |     |
| 380   | 385                     | 390 |     |  |     |
| Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala |                         |     |     |  |     |
| 395   | 400                     | 405 |     |  |     |
| Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn |                         |     |     |  |     |
| 410   | 415                     | 420 |     |  |     |
| Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys |                         |     |     |  |     |
| 425   | 430                     | 435 |     |  |     |
| Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys |                         |     |     |  |     |
| 440   | 445                     | 450 |     |  |     |
| Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln |                         |     |     |  |     |
| 455   | 460                     | 465 |     |  |     |
| Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly |                         |     |     |  |     |
| 470   | 475                     | 480 |     |  |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ile | Phe | Ala | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp | 485 | 490 | 495 |
| Phe | Pro | Lys | Pro | Gln | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala | 500 | 505 | 510 |
| Ile | Lys | Gly | Ser | Asn | Leu | Ser | Phe | Ile | Cys | Ser | Ala | Ala | Ser | Ser | 515 | 520 | 525 |
| Ser | Asp | Ser | Pro | Met | Thr | Phe | Ala | Trp | Lys | Lys | Asp | Asn | Glu | Leu | 530 | 535 | 540 |
| Leu | His | Asp | Ala | Glu | Met | Glu | Asn | Tyr | Ala | His | Leu | Arg | Ala | Gln | 545 | 550 | 555 |
| Gly | Gly | Glu | Val | Met | Glu | Tyr | Thr | Thr | Ile | Leu | Arg | Leu | Arg | Glu | 560 | 565 | 570 |
| Val | Glu | Phe | Ala | Ser | Glu | Gly | Lys | Tyr | Gln | Cys | Val | Ile | Ser | Asn | 575 | 580 | 585 |
| His | Phe | Gly | Ser | Ser | Tyr | Ser | Val | Lys | Ala | Lys | Leu | Thr | Val | Asn | 590 | 595 | 600 |
| Met | Leu | Pro | Ser | Phe | Thr | Lys | Thr | Pro | Met | Asp | Leu | Thr | Ile | Arg | 605 | 610 | 615 |
| Ala | Gly | Ala | Met | Ala | Arg | Leu | Glu | Cys | Ala | Ala | Val | Gly | His | Pro | 620 | 625 | 630 |
| Ala | Pro | Gln | Ile | Ala | Trp | Gln | Lys | Asp | Gly | Gly | Thr | Asp | Phe | Pro | 635 | 640 | 645 |
| Ala | Ala | Arg | Glu | Arg | Arg | Met | His | Val | Met | Pro | Glu | Asp | Asp | Val | 650 | 655 | 660 |
| Phe | Phe | Ile | Val | Asp | Val | Lys | Ile | Glu | Asp | Ile | Gly | Val | Tyr | Ser | 665 | 670 | 675 |
| Cys | Thr | Ala | Gln | Asn | Ser | Ala | Gly | Ser | Ile | Ser | Ala | Asn | Ala | Thr | 680 | 685 | 690 |
| Leu | Thr | Val | Leu | Glu | Thr | Pro | Ser | Phe | Leu | Arg | Pro | Leu | Leu | Asp | 695 | 700 | 705 |
| Arg | Thr | Val | Thr | Lys | Gly | Glu | Thr | Ala | Val | Leu | Gln | Cys | Ile | Ala | 710 | 715 | 720 |
| Gly | Gly | Ser | Pro | Pro | Pro | Lys | Leu | Asn | Trp | Thr | Lys | Asp | Asp | Ser | 725 | 730 | 735 |
| Pro | Leu | Val | Val | Thr | Glu | Arg | His | Phe | Phe | Ala | Ala | Gly | Asn | Gln | 740 | 745 | 750 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|
| Leu | Leu | Ile | Ile | Val | Asp | Ser | Asp | Val | Ser | Asp | Ala | Gly | Lys | Tyr | 755 | 760  | 765  |
| Thr | Cys | Glu | Met | Ser | Asn | Thr | Leu | Gly | Thr | Glu | Arg | Gly | Asn | Val | 770 | 775  | 780  |
| Arg | Leu | Ser | Val | Ile | Pro | Thr | Pro | Thr | Cys | Asp | Ser | Pro | Gln | Met | 785 | 790  | 795  |
| Thr | Ala | Pro | Ser | Leu | Asp | Asp | Asp | Gly | Trp | Ala | Thr | Val | Gly | Val | 800 | 805  | 810  |
| Val | Ile | Ile | Ala | Val | Val | Cys | Cys | Val | Val | Gly | Thr | Ser | Leu | Val | 815 | 820  | 825  |
| Trp | Val | Val | Ile | Ile | Tyr | His | Thr | Arg | Arg | Arg | Asn | Glu | Asp | Cys | 830 | 835  | 840  |
| Ser | Ile | Thr | Asn | Thr | Asp | Glu | Thr | Asn | Leu | Pro | Ala | Asp | Ile | Pro | 845 | 850  | 855  |
| Ser | Tyr | Leu | Ser | Ser | Gln | Gly | Thr | Leu | Ala | Asp | Arg | Gln | Asp | Gly | 860 | 865  | 870  |
| Tyr | Val | Ser | Ser | Glu | Ser | Gly | Ser | His | His | Gln | Phe | Val | Thr | Ser | 875 | 880  | 885  |
| Ser | Gly | Ala | Gly | Phe | Phe | Leu | Pro | Gln | His | Asp | Ser | Ser | Gly | Thr | 890 | 895  | 900  |
| Cys | His | Ile | Asp | Asn | Ser | Ser | Glu | Ala | Asp | Val | Glu | Ala | Ala | Thr | 905 | 910  | 915  |
| Asp | Leu | Phe | Leu | Cys | Pro | Phe | Leu | Gly | Ser | Thr | Gly | Pro | Met | Tyr | 920 | 925  | 930  |
| Leu | Lys | Gly | Asn | Val | Tyr | Gly | Ser | Asp | Pro | Phe | Glu | Thr | Tyr | His | 935 | 940  | 945  |
| Thr | Gly | Cys | Ser | Pro | Asp | Pro | Arg | Thr | Val | Leu | Met | Asp | His | Tyr | 950 | 955  | 960  |
| Glu | Pro | Ser | Tyr | Ile | Lys | Lys | Lys | Glu | Cys | Tyr | Pro | Cys | Ser | His | 965 | 970  | 975  |
| Pro | Ser | Glu | Glu | Ser | Cys | Glu | Arg | Ser | Phe | Ser | Asn | Ile | Ser | Trp | 980 | 985  | 990  |
| Pro | Ser | His | Val | Arg | Lys | Leu | Leu | Asn | Thr | Ser | Tyr | Ser | His | Asn | 995 | 1000 | 1005 |
| Glu | Gly | Pro | Gly | Met | Lys | Asn | Leu | Cys | Leu | Asn | Lys | Ser | Ser | Leu |     |      |      |

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| 1010  | 1015 | 1020 |
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| Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn |      |      |
| 1025  | 1030 | 1035 |
| Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu |      |      |
| 1040  | 1045 | 1050 |
| Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg |      |      |
| 1055  | 1060 | 1065 |
| Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly |      |      |
| 1070  | 1075 | 1080 |
| Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn |      |      |
| 1085  | 1090 | 1095 |
| His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro |      |      |
| 1100  | 1105 | 1110 |
| Asn Phe Gln Ser Tyr Asp Leu Asp Thr                         |      |      |
| 1115  |      |      |

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&lt;223&gt; Synthetic Oligonucleotide Probe

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&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Synthetic Oligonucleotide Probe

FOOTNOTES 65220660

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<211> 45

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<223> Synthetic Oligonucleotide Probe

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gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcgc 400

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Asp | Phe | Leu | Leu | Ala | Leu | Val | Leu | Val | Ser | Ser | Leu | Tyr | Leu | 1   | 5   | 10  | 15 |
| Gln | Ala | Ala | Ala | Glu | Phe | Asp | Gly | Arg | Trp | Pro | Arg | Gln | Ile | Val | 20  | 25  | 30  |    |
| Ser | Ser | Ile | Gly | Leu | Cys | Arg | Tyr | Gly | Gly | Arg | Ile | Asp | Cys | Cys | 35  | 40  | 45  |    |
| Trp | Gly | Trp | Ala | Arg | Gln | Ser | Trp | Gly | Gln | Cys | Gln | Pro | Val | Cys | 50  | 55  | 60  |    |
| Gln | Pro | Arg | Cys | Lys | His | Gly | Glu | Cys | Ile | Gly | Pro | Asn | Lys | Cys | 65  | 70  | 75  |    |
| Lys | Cys | His | Pro | Gly | Tyr | Ala | Gly | Lys | Thr | Cys | Asn | Gln | Asp | Leu | 80  | 85  | 90  |    |
| Asn | Glu | Cys | Gly | Leu | Lys | Pro | Arg | Pro | Cys | Lys | His | Arg | Cys | Met | 95  | 100 | 105 |    |
| Asn | Thr | Tyr | Gly | Ser | Tyr | Lys | Cys | Tyr | Cys | Leu | Asn | Gly | Tyr | Met | 110 | 115 | 120 |    |
| Leu | Met | Pro | Asp | Gly | Ser | Cys | Ser | Ser | Ala | Leu | Thr | Cys | Ser | Met | 125 | 130 | 135 |    |
| Ala | Asn | Cys | Gln | Tyr | Gly | Cys | Asp | Val | Val | Lys | Gly | Gln | Ile | Arg | 140 | 145 | 150 |    |
| Cys | Gln | Cys | Pro | Ser | Pro | Gly | Leu | His | Leu | Ala | Pro | Asp | Gly | Arg | 155 | 160 | 165 |    |

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|                 |                     |                         |
|-----------------|---------------------|-------------------------|
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| 170             |                     | 175 180                 |
| Pro Arg Phe Arg | Gln Cys Val Asn Thr | Phe Gly Ser Tyr Ile Cys |
| 185             |                     | 190 195                 |
| Lys Cys His Lys | Gly Phe Asp Leu Met | Tyr Ile Gly Gly Lys Tyr |
| 200             |                     | 205 210                 |
| Gln Cys His Asp | Ile Asp Glu Cys Ser | Leu Gly Gln Tyr Gln Cys |
| 215             |                     | 220 225                 |
| Ser Ser Phe Ala | Arg Cys Tyr Asn Val | Arg Gly Ser Tyr Lys Cys |
| 230             |                     | 235 240                 |
| Lys Cys Lys Glu | Gly Tyr Gln Gly Asp | Gly Leu Thr Cys Val Tyr |
| 245             |                     | 250 255                 |
| Ile Pro Lys Val | Met Ile Glu Pro Ser | Gly Pro Ile His Val Pro |
| 260             |                     | 265 270                 |
| Lys Gly Asn Gly | Thr Ile Leu Lys Gly | Asp Thr Gly Asn Asn Asn |
| 275             |                     | 280 285                 |
| Trp Ile Pro Asp | Val Gly Ser Thr Trp | Trp Pro Pro Lys Thr Pro |
| 290             |                     | 295 300                 |
| Tyr Ile Pro Pro | Ile Ile Thr Asn Arg | Pro Thr Ser Lys Pro Thr |
| 305             |                     | 310 315                 |
| Thr Arg Pro Thr | Pro Lys Pro Thr Pro | Ile Pro Thr Pro Pro Pro |
| 320             |                     | 325 330                 |
| Pro Pro Pro Leu | Pro Thr Glu Leu Arg | Thr Pro Leu Pro Pro Thr |
| 335             |                     | 340 345                 |
| Thr Pro Glu Arg | Pro Thr Thr Gly Leu | Thr Thr Ile Ala Pro Ala |
| 350             |                     | 355 360                 |
| Ala Ser Thr Pro | Pro Gly Gly Ile Thr | Val Asp Asn Arg Val Gln |
| 365             |                     | 370 375                 |
| Thr Asp Pro Gln | Lys Pro Arg Gly Asp | Val Phe Ser Val Leu Val |
| 380             |                     | 385 390                 |
| His Ser Cys Asn | Phe Asp His Gly Leu | Cys Gly Trp Ile Arg Glu |
| 395             |                     | 400 405                 |
| Lys Asp Asn Asp | Leu His Trp Glu Pro | Ile Arg Asp Pro Ala Gly |
| 410             |                     | 415 420                 |
| Gly Gln Tyr Leu | Thr Val Ser Ala Ala | Lys Ala Pro Gly Gly Lys |

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|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 425 |  | 430 |  | 435 |
| Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly |     |  |     |  |     |
|   | 440 |  | 445 |  | 450 |
| Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser |     |  |     |  |     |
|   | 455 |  | 460 |  | 465 |
| Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala |     |  |     |  |     |
|   | 470 |  | 475 |  | 480 |
| Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln |     |  |     |  |     |
|   | 485 |  | 490 |  | 495 |
| Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg     |     |  |     |  |     |
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&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

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&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

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&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

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&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

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<213> Homo Sapien

<400> 319

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0990239 074001



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<213> Homo Sapien

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| Met | Trp | Leu | Lys | Val | Phe | Thr | Thr | Phe | Leu | Ser | Phe | Ala | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Cys | Ser | Gly | Leu | Lys | Val | Thr | Val | Pro | Ser | His | Thr | Val | His |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Arg | Gly | Gln | Ala | Leu | Tyr | Leu | Pro | Val | His | Tyr | Gly | Phe |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Pro | Ala | Ser | Asp | Ile | Gln | Ile | Ile | Trp | Leu | Phe | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | His | Thr | Met | Pro | Lys | Tyr | Leu | Leu | Gly | Ser | Val | Asn | Lys | Ser |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Val | Val | Pro | Asp | Leu | Glu | Tyr | Gln | His | Lys | Phe | Thr | Met | Met | Pro |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Pro | Asn | Ala | Ser | Leu | Leu | Ile | Asn | Pro | Leu | Gln | Phe | Pro | Asp | Glu |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Gly | Asn | Tyr | Ile | Val | Lys | Val | Asn | Ile | Gln | Gly | Asn | Gly | Thr | Leu |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Ser | Ala | Ser | Gln | Lys | Ile | Gln | Val | Thr | Val | Asp | Asp | Pro | Val | Thr |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |
| Lys | Pro | Val | Val | Gln | Ile | His | Pro | Pro | Ser | Gly | Ala | Val | Glu | Tyr |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |  |
| Val | Gly | Asn | Met | Thr | Leu | Thr | Cys | His | Val | Glu | Gly | Gly | Thr | Arg |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |  |
| Leu | Ala | Tyr | Gln | Trp | Leu | Lys | Asn | Gly | Arg | Pro | Val | His | Thr | Ser |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |  |
| Ser | Thr | Tyr | Ser | Phe | Ser | Pro | Gln | Asn | Asn | Thr | Leu | His | Ile | Ala |  |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |  |
| Pro | Val | Thr | Lys | Glu | Asp | Ile | Gly | Asn | Tyr | Ser | Cys | Leu | Val | Arg |  |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |  |
| Asn | Pro | Val | Ser | Glu | Met | Glu | Ser | Asp | Ile | Ile | Met | Pro | Ile | Ile |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |  |
| Tyr | Tyr | Gly | Pro | Tyr | Gly | Leu | Gln | Val | Asn | Ser | Asp | Lys | Gly | Leu |  |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Lys | Val | Gly | Glu | Val | Phe | Thr | Val | Asp | Leu | Gly | Glu | Ala | Ile | Leu |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |  |
| Phe | Asp | Cys | Ser | Ala | Asp | Ser | His | Pro | Pro | Asn | Thr | Tyr | Ser | Trp |  |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |  |
| Ile | Arg | Arg | Thr | Asp | Asn | Thr | Thr | Tyr | Ile | Ile | Lys | His | Gly | Pro |  |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |  |
| Arg | Leu | Glu | Val | Ala | Ser | Glu | Lys | Val | Ala | Gln | Lys | Thr | Met | Asp |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Tyr | Val | Cys | Cys | Ala | Tyr | Asn | Asn | Ile | Thr | Gly | Arg | Gln | Asp | Glu |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |  |
| Thr | His | Phe | Thr | Val | Ile | Ile | Thr | Ser | Val | Gly | Leu | Glu | Lys | Leu |  |

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|   | 320 | 325 | 330 |
|---|-----|-----|-----|
| Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly | 335 | 340 | 345 |
| Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp | 350 | 355 | 360 |
| Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly | 365 | 370 | 375 |
| Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His | 380 | 385 | 390 |
| Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe | 395 | 400 | 405 |
| Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro | 410 | 415 | 420 |
| Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr | 425 | 430 | 435 |
| Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu | 440 | 445 | 450 |

&lt;210&gt; 321

&lt;211&gt; 25

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

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&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

FOOT-0-5520560

<220>

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<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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20 25 30

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35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 215 |     | 220 |     | 225 |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Ser | Ala | Gln | Pro | Leu | Lys | Lys | Val | Glu | Glu | Glu | Gln | Glu |
|     | 230 |     |     |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Asp | Glu | Glu | Asp | Val | Ser | Glu | Glu | Glu | Ala | Glu | Ser | Lys | Glu |
|     | 245 |     |     |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Gly | Thr | Asn | Lys | Asp | Phe | Pro | Gln | Asn | Ala | Ile | Arg | Gln | Arg | Ser |
|     | 260 |     |     |     |     |     |     |     | 265 |     |     |     |     | 270 |
| Leu | Gly | Pro | Ser | Leu | Ala | Thr | Asp | Lys | Ser |     |     |     |     |     |
|     | 275 |     |     |     |     |     |     |     | 280 |     |     |     |     |     |

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

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&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

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&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

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&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 329

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<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

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<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

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ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

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<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Trp | Val | Ser | Ala | Leu | Leu | Met | Ala | Trp | Phe | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Cys | Val | Gln | Ala | Glu | Phe | Phe | Thr | Ser | Ile | Gly | His | Met |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Leu | Ile | Tyr | Ala | Glu | Lys | Glu | Leu | Val | Gln | Ser | Leu | Lys |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Tyr | Ile | Leu | Val | Glu | Glu | Ala | Lys | Leu | Ser | Lys | Ile | Lys | Ser |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Asn | Lys | Met | Glu | Ala | Leu | Thr | Ser | Lys | Ser | Ala | Ala | Asp |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Gly | Tyr | Leu | Ala | His | Pro | Val | Asn | Ala | Tyr | Lys | Leu | Val |
|     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Leu | Asn | Thr | Asp | Trp | Pro | Ala | Leu | Glu | Asp | Leu | Val | Leu |
|     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |     | 105 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Ser | Ala | Ala | Gly | Phe | Ile | Ala | Asn | Leu | Ser | Val | Gln | Arg |
|     |     |     | 110 |     |     |     |     |     | 115 |     |     |     |     | 120 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Phe | Phe | Pro | Thr | Asp | Glu | Asp | Glu | Ile | Gly | Ala | Ala | Lys | Ala |
|     |     |     | 125 |     |     |     |     |     | 130 |     |     |     |     | 135 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Met | Arg | Leu | Gln | Asp | Thr | Tyr | Arg | Leu | Asp | Pro | Gly | Thr | Ile |
|     |     |     | 140 |     |     |     |     |     | 145 |     |     |     |     | 150 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Gly | Glu | Leu | Pro | Gly | Thr | Lys | Tyr | Gln | Ala | Met | Leu | Ser |
|     |     |     | 155 |     |     |     |     |     | 160 |     |     |     |     | 165 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Asp | Cys | Phe | Gly | Met | Gly | Arg | Ser | Ala | Tyr | Asn | Glu | Gly |
|     |     |     | 170 |     |     |     |     |     | 175 |     |     |     |     | 180 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Tyr | His | Thr | Val | Leu | Trp | Met | Glu | Gln | Val | Leu | Lys | Gln |
|     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |     | 195 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Ala | Gly | Glu | Glu | Ala | Thr | Thr | Thr | Lys | Ser | Gln | Val | Leu |
|     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     | 210 |

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|                 |   |     |     |     |
|-----------------|---|-----|-----|-----|
| Asp Tyr Leu Ser | Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg | 215 | 220 | 225 |
| Ala Leu Glu Leu | Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His | 230 | 235 | 240 |
| Glu Arg Ala Gly | Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu | 245 | 250 | 255 |
| Glu Glu Arg Glu | Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu | 260 | 265 | 270 |
| Ala Thr Pro Glu | Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro | 275 | 280 | 285 |
| Glu Arg Asp Val | Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys | 290 | 295 | 300 |
| Leu Thr Pro Arg | Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His | 305 | 310 | 315 |
| Gly Asn Arg Ala | Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu | 320 | 325 | 330 |
| Asp Glu Trp Asp | Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met | 335 | 340 | 345 |
| Ser Asp Glu Glu | Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys | 350 | 355 | 360 |
| Leu Ala Arg Ala | Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr | 365 | 370 | 375 |
| Val Ala Ser Tyr | Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp | 380 | 385 | 390 |
| Asp Asp Pro Val | Val Ala Arg Val Asn Arg Arg Met Gln His Ile | 395 | 400 | 405 |
| Thr Gly Leu Thr | Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn | 410 | 415 | 420 |
| Tyr Gly Val Gly | Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg | 425 | 430 | 435 |
| Arg Pro Phe Asp | Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala | 440 | 445 | 450 |
| Thr Phe Leu Asn | Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr | 455 | 460 | 465 |
| Val Phe Pro Asp | Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr | 470 | 475 | 480 |

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Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
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<211> 18

<212> DNA

<213> Artificial Sequence

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<400> 333

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<210> 334

<211> 19

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<210> 336

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<400> 336  
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<211> 2789

<212> DNA

<213> Homo Sapien

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<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Arg | Pro | Ala | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Gly | Leu | Ser | Leu | Gly | Cys | Ser | Leu | Ser | Leu | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Trp | Ile | Gln | Gly | Glu | Gly | Glu | Asp | Pro | Cys | Val | Glu | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Arg | Gly | Gly | Pro | Gln | Asn | Pro | Asp | Ser | Arg | Ala | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | Ser | Asp | Glu | Asp | Phe | Lys | Pro | Arg | Ile | Val | Pro | Tyr |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Asp | Pro | Asn | Lys | Pro | Tyr | Lys | Lys | Val | Leu | Arg | Thr | Arg |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Gln | Thr | Glu | Leu | Gly | Ser | Arg | Glu | Arg | Leu | Leu | Val | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|                 |                         |                         |     |  |     |
|-----------------|-------------------------|-------------------------|-----|--|-----|
|                 | 95                      |                         | 100 |  | 105 |
| Val Leu Thr Ser | Arg Ala Thr Leu Ser     | Thr Leu Ala Val Ala Val |     |  |     |
|                 | 110                     | 115                     |     |  | 120 |
| Asn Arg Thr Val | Ala His His Phe Pro Arg | Leu Leu Tyr Phe Thr     |     |  |     |
|                 | 125                     | 130                     |     |  | 135 |
| Gly Gln Arg Gly | Ala Arg Ala Pro Ala Gly | Met Gln Val Val Ser     |     |  |     |
|                 | 140                     | 145                     |     |  | 150 |
| His Gly Asp Glu | Arg Pro Ala Trp Leu Met | Ser Glu Thr Leu Arg     |     |  |     |
|                 | 155                     | 160                     |     |  | 165 |
| His Leu His Thr | His Phe Gly Ala Asp Tyr | Asp Trp Phe Phe Ile     |     |  |     |
|                 | 170                     | 175                     |     |  | 180 |
| Met Gln Asp Asp | Thr Tyr Val Gln Ala Pro | Arg Leu Ala Ala Leu     |     |  |     |
|                 | 185                     | 190                     |     |  | 195 |
| Ala Gly His Leu | Ser Ile Asn Gln Asp Leu | Tyr Leu Gly Arg Ala     |     |  |     |
|                 | 200                     | 205                     |     |  | 210 |
| Glu Glu Phe Ile | Gly Ala Gly Glu Gln Ala | Arg Tyr Cys His Gly     |     |  |     |
|                 | 215                     | 220                     |     |  | 225 |
| Gly Phe Gly Tyr | Leu Leu Ser Arg Ser Leu | Leu Leu Arg Leu Arg     |     |  |     |
|                 | 230                     | 235                     |     |  | 240 |
| Pro His Leu Asp | Gly Cys Arg Gly Asp Ile | Leu Ser Ala Arg Pro     |     |  |     |
|                 | 245                     | 250                     |     |  | 255 |
| Asp Glu Trp Leu | Gly Arg Cys Leu Ile Asp | Ser Leu Gly Val Gly     |     |  |     |
|                 | 260                     | 265                     |     |  | 270 |
| Cys Val Ser Gln | His Gln Gly Gln Gln Tyr | Arg Ser Phe Glu Leu     |     |  |     |
|                 | 275                     | 280                     |     |  | 285 |
| Ala Lys Asn Arg | Asp Pro Glu Lys Glu Gly | Ser Ser Ala Phe Leu     |     |  |     |
|                 | 290                     | 295                     |     |  | 300 |
| Ser Ala Phe Ala | Val His Pro Val Ser Glu | Gly Thr Leu Met Tyr     |     |  |     |
|                 | 305                     | 310                     |     |  | 315 |
| Arg Leu His Lys | Arg Phe Ser Ala Leu Glu | Leu Glu Arg Ala Tyr     |     |  |     |
|                 | 320                     | 325                     |     |  | 330 |
| Ser Glu Ile Glu | Gln Leu Gln Ala Gln Ile | Arg Asn Leu Thr Val     |     |  |     |
|                 | 335                     | 340                     |     |  | 345 |
| Leu Thr Pro Glu | Gly Glu Ala Gly Leu Ser | Trp Pro Val Gly Leu     |     |  |     |
|                 | 350                     | 355                     |     |  | 360 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Pro | Phe | Thr | Pro | His | Ser | Arg | Phe | Glu | Val | Leu | Gly | Trp | 365 | 370 | 375 |
| Asp | Tyr | Phe | Thr | Glu | Gln | His | Thr | Phe | Ser | Cys | Ala | Asp | Gly | Ala | 380 | 385 | 390 |
| Pro | Lys | Cys | Pro | Leu | Gln | Gly | Ala | Ser | Arg | Ala | Asp | Val | Gly | Asp | 395 | 400 | 405 |
| Ala | Leu | Glu | Thr | Ala | Leu | Glu | Gln | Leu | Asn | Arg | Arg | Tyr | Gln | Pro | 410 | 415 | 420 |
| Arg | Leu | Arg | Phe | Gln | Lys | Gln | Arg | Leu | Leu | Asn | Gly | Tyr | Arg | Arg | 425 | 430 | 435 |
| Phe | Asp | Pro | Ala | Arg | Gly | Met | Glu | Tyr | Thr | Leu | Asp | Leu | Leu | Leu | 440 | 445 | 450 |
| Glu | Cys | Val | Thr | Gln | Arg | Gly | His | Arg | Arg | Ala | Leu | Ala | Arg | Arg | 455 | 460 | 465 |
| Val | Ser | Leu | Leu | Arg | Pro | Leu | Ser | Arg | Val | Glu | Ile | Leu | Pro | Met | 470 | 475 | 480 |
| Pro | Tyr | Val | Thr | Glu | Ala | Thr | Arg | Val | Gln | Leu | Val | Leu | Pro | Leu | 485 | 490 | 495 |
| Leu | Val | Ala | Glu | Ala | Ala | Ala | Ala | Pro | Ala | Phe | Leu | Glu | Ala | Phe | 500 | 505 | 510 |
| Ala | Ala | Asn | Val | Leu | Glu | Pro | Arg | Glu | His | Ala | Leu | Leu | Thr | Leu | 515 | 520 | 525 |
| Leu | Leu | Val | Tyr | Gly | Pro | Arg | Glu | Gly | Gly | Arg | Gly | Ala | Pro | Asp | 530 | 535 | 540 |
| Pro | Phe | Leu | Gly | Val | Lys | Ala | Ala | Ala | Ala | Glu | Leu | Glu | Arg | Arg | 545 | 550 | 555 |
| Tyr | Pro | Gly | Thr | Arg | Leu | Ala | Trp | Leu | Ala | Val | Arg | Ala | Glu | Ala | 560 | 565 | 570 |
| Pro | Ser | Gln | Val | Arg | Leu | Met | Asp | Val | Val | Ser | Lys | Lys | His | Pro | 575 | 580 | 585 |
| Val | Asp | Thr | Leu | Phe | Phe | Leu | Thr | Thr | Val | Trp | Thr | Arg | Pro | Gly | 590 | 595 | 600 |
| Pro | Glu | Val | Leu | Asn | Arg | Cys | Arg | Met | Asn | Ala | Ile | Ser | Gly | Trp | 605 | 610 | 615 |
| Gln | Ala | Phe | Phe | Pro | Val | His | Phe | Gln | Glu | Phe | Asn | Pro | Ala | Leu | 620 | 625 | 630 |

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Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
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 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
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 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
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gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
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<211> 318

<212> PRT

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&lt;400&gt; 341

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| Met | Leu | Ser | Glu | Ser | Ser | Ser | Phe | Leu | Lys | Gly | Val | Met | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Ser | Ile | Phe | Cys | Ala | Leu | Ile | Thr | Met | Leu | Gly | His | Ile | Arg | Ile |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Gly | His | Gly | Asn | Arg | Met | His | His | His | Glu | His | His | His | Leu | Gln |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Ala | Pro | Asn | Lys | Glu | Asp | Ile | Leu | Lys | Ile | Ser | Glu | Asp | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Met | Glu | Leu | Ser | Lys | Ser | Phe | Arg | Val | Tyr | Cys | Ile | Ile | Leu | Val |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Lys | Pro | Lys | Asp | Val | Ser | Leu | Trp | Ala | Ala | Val | Lys | Glu | Thr | Trp |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Thr | Lys | His | Cys | Asp | Lys | Ala | Glu | Phe | Phe | Ser | Ser | Glu | Asn | Val |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Lys | Val | Phe | Glu | Ser | Ile | Asn | Met | Asp | Thr | Asn | Asp | Met | Trp | Leu |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Met | Met | Arg | Lys | Ala | Tyr | Lys | Tyr | Ala | Phe | Asp | Lys | Tyr | Arg | Asp |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Gln | Tyr | Asn | Trp | Phe | Phe | Leu | Ala | Arg | Pro | Thr | Thr | Phe | Ala | Ile |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Ile | Glu | Asn | Leu | Lys | Tyr | Phe | Leu | Leu | Lys | Lys | Asp | Pro | Ser | Gln |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| Pro | Phe | Tyr | Leu | Gly | His | Thr | Ile | Lys | Ser | Gly | Asp | Leu | Glu | Tyr |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |
| Val | Gly | Met | Glu | Gly | Gly | Ile | Val | Leu | Ser | Val | Glu | Ser | Met | Lys |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |
| Arg | Leu | Asn | Ser | Leu | Leu | Asn | Ile | Pro | Glu | Lys | Cys | Pro | Glu | Gln |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Gly | Gly | Met | Ile | Trp | Lys | Ile | Ser | Glu | Asp | Lys | Gln | Leu | Ala | Val |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Cys | Leu | Lys | Tyr | Ala | Gly | Val | Phe | Ala | Glu | Asn | Ala | Glu | Asp | Ala |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Gly | Lys | Asp | Val | Phe | Asn | Thr | Lys | Ser | Val | Gly | Leu | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |

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|---------------------|-------------------------|---------------------|-----|--|-----|
|                     | 260                     |                     | 265 |  | 270 |
| Cys Ser Asp Met     | Ala Val Thr Phe Asn Gly | Leu Thr Pro Asn Gln |     |  |     |
|                     | 275                     |                     | 280 |  | 285 |
| Met His Val Met     | Met Tyr Gly Val Tyr Arg | Leu Arg Ala Phe Gly |     |  |     |
|                     | 290                     |                     | 295 |  | 300 |
| His Ile Phe Asn Asp | Ala Leu Val Phe Leu     | Pro Pro Asn Gly Ser |     |  |     |
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<220>

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<400> 349

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<400> 367

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<211> 47

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<210> 369

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<210> 371

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<223> Synthetic Oligonucleotide Probe

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<213> Homo Sapien

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| agggaggggag | agaaaaagag  | agagagagaa  | acaaaaaacc | aaagagagag | 100 |
| aaaaaatgaa  | ttcatctaaa  | tcatctgaaa  | cacaatgcac | agagagagga | 150 |
| tgcttctctt  | cccaaagtgt  | cttatggact  | gttgctggga | tccccatcct | 200 |
| atcttctcagt | gcctgtttca  | tcaccagatg  | tgttgtgaca | tttcgcatct | 250 |
| ttcaaacctg  | tgatgagaaa  | aagtttcagc  | tacctgagaa | tttcacagag | 300 |
| ctctcctgct  | acaattatgg  | atcaggttca  | gtcaagaatt | gttgtccatt | 350 |
| gaactgggaa  | tatttttcaat | ccagctgcta  | cttcttttct | actgacacca | 400 |
| tttctctgggc | gttaagttta  | aagaactgct  | cagccatggg | ggctcacctg | 450 |
| gtggttatca  | actcacagga  | ggagcaggaa  | ttccttttct | acaagaaacc | 500 |
| taaaatgaga  | gagtttttta  | ttggactgtc  | agaccagggt | gtcgagggtc | 550 |
| agtggcaatg  | ggtggacggc  | acacctttga  | caaagtctct | gagcttctgg | 600 |
| gatgtagggg  | agcccaacaa  | catagctacc  | ctggaggact | gtgccaccat | 650 |
| gagagactct  | tcaaacccaa  | ggcaaaattg  | gaatgatgta | acctgtttcc | 700 |
| tcaattattt  | tcggatttgt  | gaaatggtag  | gaataaatcc | tttgaacaaa | 750 |

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 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
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<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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| Met | Asn | Ser | Ser | Lys | Ser | Ser | Glu | Thr | Gln | Cys | Thr | Glu | Arg | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Cys | Phe | Ser | Ser | Gln | Met | Phe | Leu | Trp | Thr | Val | Ala | Gly | Ile | Pro |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |
| Ile | Leu | Phe | Leu | Ser | Ala | Cys | Phe | Ile | Thr | Arg | Cys | Val | Val | Thr |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |
| Phe | Arg | Ile | Phe | Gln | Thr | Cys | Asp | Glu | Lys | Lys | Phe | Gln | Leu | Pro |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
| Glu | Asn | Phe | Thr | Glu | Leu | Ser | Cys | Tyr | Asn | Tyr | Gly | Ser | Gly | Ser |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Val | Lys | Asn | Cys | Cys | Pro | Leu | Asn | Trp | Glu | Tyr | Phe | Gln | Ser | Ser |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Cys | Tyr | Phe | Phe | Ser | Thr | Asp | Thr | Ile | Ser | Trp | Ala | Leu | Ser | Leu |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Lys | Asn | Cys | Ser | Ala | Met | Gly | Ala | His | Leu | Val | Val | Ile | Asn | Ser |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Gln | Glu | Glu | Gln | Glu | Phe | Leu | Ser | Tyr | Lys | Lys | Pro | Lys | Met | Arg |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |
| Glu | Phe | Phe | Ile | Gly | Leu | Ser | Asp | Gln | Val | Val | Glu | Gly | Gln | Trp |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |  |
| Gln | Trp | Val | Asp | Gly | Thr | Pro | Leu | Thr | Lys | Ser | Leu | Ser | Phe | Trp |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |  |
| Asp | Val | Gly | Glu | Pro | Asn | Asn | Ile | Ala | Thr | Leu | Glu | Asp | Cys | Ala |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |  |

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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
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Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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tgccagctgc atgctgccag tt 22

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| Pro | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly |
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| Ala | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Phe | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Ser | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Thr | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Arg | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Thr | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg |
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|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Gln | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val |
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| Pro | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly |
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| His | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu |
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